

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:49:23 ; Search time 46 Seconds
(without alignments)
1897.373 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTSPSSSTALASCRIARR.....SQEASQTLLDSVYSHLPDLL 655

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_101002.*

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	100.0	655	AA1983	Human PRO868 prote
2	655	100.0	655	AA1984	Novel human tumor
3	655	100.0	655	AA1985	Human tumor necro
4	655	100.0	655	AA1986	Tumour necrosis fa
5	655	100.0	655	AA1987	DR-6 death recepto
6	655	100.0	655	AA1988	Human TNF receptor
7	655	100.0	655	AA1989	Human PRO polypept
8	655	100.0	655	AA1990	Human death domain
9	655	100.0	655	AA1991	Human osteoprotegr
10	631	96.3	631	AA1992	Human full-length

11	631	96.3	631	AAE21959	Human death domain
12	631	96.3	655	AAW75792	Human tumour necro
13	554	84.6	655	AAW75792	Human PRO868 (UNO4
14	544	83.1	605	AAW75792	Human TNF receptor
15	541	82.6	605	AAW75792	Human protein sequ
16	479	73.1	508	AAW75792	Tumour necrosis fa
17	415	63.4	444	AAW75792	Human TNF receptor
18	405	61.8	405	AAW75792	Human DTH protein
19	326	49.8	393	AAW75792	A human tumour nec
20	250	38.2	254	AAW75792	Human osteoprotegr
21	249	38.0	253	AAW75792	Human TNF receptor
22	225	34.4	229	AAW75792	Human soluble tumo
23	218	33.3	222	AAW75792	Human brain expres
24	218	33.3	222	AAW75792	Peptide #3246 enco
25	218	33.3	222	AAW75792	Peptide #3331 enco
26	218	33.3	222	AAW75792	Peptide #3210 enco
27	218	33.3	222	AAW75792	Human peptide enco
28	184	28.1	290	AAW75792	Human osteoprotegr
29	184	28.1	290	AAW75792	Human osteoprotegr
30	164	25.0	164	AAW75792	Peptide fragment o
31	125	19.1	125	AAW75792	Tumour necrosis fa
32	119	18.2	147	AAW75792	Human TNF receptor
33	116	17.7	573	AAW75792	Mouse TNF receptor
34	116	17.7	600	AAW75792	Murine osteoprotegr
35	86	13.1	210	AAW75792	Human TNF receptor
36	85	13.0	85	AAW75792	Peptide #1969 enco
37	85	13.0	85	AAW75792	Peptide #3406 enco
38	85	13.0	85	AAW75792	Peptide #3438 enco
39	85	13.0	85	AAW75792	Protein #1900 enco
40	85	13.0	85	AAW75792	Protein #3340 enco
41	85	13.0	85	AAW75792	Human brain expres
42	85	13.0	85	AAW75792	Human brain expres
43	85	13.0	85	AAW75792	Human bone marrow
44	85	13.0	85	AAW75792	Human bone marrow
45	85	13.0	85	AAW75792	Peptide #1918 enco

ALIGNMENTS

RESULT 1

AA1983
ID AA1983 standard; Protein; 655 AA.

AC AA1983;
XX

DT 07-DEC-1999 (first entry)
XX

DE Human PRO868 protein sequence.
XX

KW Human; PRO; EST: expressed sequence tag; PCR primer; hybridisation;
XX

KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX

KW secreted protein; transmembrane protein.
XX

OS Homo sapiens.
XX

PN WO9946281-A2.
XX

PD 16-SEP-1999.
XX

PF 08-MAR-1999; 99WO-US05028.
XX

PR 10-MAR-1998; 98US-0077450.
XX

PR 11-MAR-1998; 98US-0077632.
XX

PR 11-MAR-1998; 98US-0077641.
XX

PR 12-MAR-1998; 98US-0077649.
XX

PR 13-MAR-1998; 98US-0077791.
XX

PR 17-MAR-1998; 98US-0078004.
XX

PR 20-MAR-1998; 98US-0040220.
XX

PR 20-MAR-1998; 98US-0078886.
XX

PR 20-MAR-1998; 98US-0078910.
XX

PR 20-MAR-1998; 98US-0078936.
XX

PR 20-MAR-1998; 98US-0078939.
XX

PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079669.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 09-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 29-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 26-MAY-1998; 98US-0087098.

PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX (GETH) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 XX WPI; 1999-551358/46.
 DR N-PSDB; AA233945.
 DR
 XX New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 XX
 XX
 PS Claim 12; Fig 26; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AA233891 to
 CC AA234338, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 655 AA;
 Query Match 100.0%; Score 655; DB 20; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLLGLFSTTTAAQPEQKASNLICTYRHVDRA 60
 DB 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLLGLFSTTTAAQPEQKASNLICTYRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTTRHENGIEKCHDCSQCPWPWIEK 120
 DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTTRHENGIEKCHDCSQCPWPWIEK 120
 QY 121 LPCAALTDRCTCPGCMFQSNATCAPHTVCPGVGVRKKGTTEDYRCQKARGTSDVP 180
 DB 121 LPCAALTDRCTCPGCMFQSNATCAPHTVCPGVGVRKKGTTEDYRCQKARGTSDVP 180
 QY 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 DB 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSSASVPRPKVLSIQEGTVPDNTSSARGKEDVAKTLPNLOVNH 300
 DB 241 VPSSTYVPKGMNSTESNSSASVPRPKVLSIQEGTVPDNTSSARGKEDVAKTLPNLOVNH 300
 QY 301 QOQPHRHILKLLPSMEATGGEKSSPTPIKGRGHRGPRQNLKHDFDNEHLPWIVLFLLL 360
 DB 301 QOQPHRHILKLLPSMEATGGEKSSPTPIKGRGHRGPRQNLKHDFDNEHLPWIVLFLLL 360
 QY 361 VLVIIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTTONREKWIYCNHGHDILK 420
 DB 361 VLVIIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTTONREKWIYCNHGHDILK 420
 QY 421 LVAAQVGSOWKDIYQFLCNASREVAAFNGYTAHERAYAAALQHTTIRGPASLAQLIS 480
 DB 421 LVAAQVGSOWKDIYQFLCNASREVAAFNGYTAHERAYAAALQHTTIRGPASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLSPSPSPNKLNSALITVBP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLSPSPSPNKLNSALITVBP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSSSSALSRRNGSFITKEKDTVLVRQVRLDPCDLPITF 600

|||||
Db 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKDVLQVRLDPCDLQPIF 600
Qy 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKQSEASOTLLDSVYSHLPDLL 655
Db 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKQSEASOTLLDSVYSHLPDLL 655

RESULT 2

AAW81059 standard; Protein: 655 AA.

XX AC AAW81059;

DT 10-MAY-1999 (first entry)

DE Novel human tumor necrosis factor receptor TR9.

XX Human; tumour necrosis factor receptor; TNFR; TR9 receptor; cancer;
KW apoptosis; agonist; inhibition; autoimmune disorder; viral infection;
KW inflammation; antagonist; AIDS; neurodegenerative disorder.

XX Homo sapiens.

XX FH Key Location/Qualifiers
FT Peptide 1..40

FT /note= "signal peptide"

FT Peptide 41..655

FT /note= "mature protein"

XX W09856892-A1.

XX 17-DEC-1998.

PD 10-JUN-1998; 98WO-US11932.

PR 11-JUN-1997; 97US-0052991.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Fan P, Gentz RL, Ni J, Yu G;

XX WPI; 1999-060325/05.

DR N-PSDB; AAW99927.

PT New isolated tumour necrosis factor-like receptor, TR9 - used to
PT develop products for treating e.g. cancers, autoimmune disorders,
PT viral infections, inflammation, graft rejection, neurodegenerative
PT disorders or ischaemic injury

XX Claim 1; Fig 1; 134pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor
CC receptor (TNFR), TR9 receptor, used in the method of the invention
CC to develop products to treat disorders such as cancers. The novel
CC TNFR, TR9, can be used to identify agents for modifying apoptosis.
CC Agonists can be used to treat diseases associated with increased
CC cell survival, or the inhibition of apoptosis, including cancers
CC (e.g. follicular lymphomas, carcinomas with p53 mutations, and
CC hormone-dependent tumours, such as breast cancer, prostate cancer,
CC Kaposi's sarcoma and ovarian cancer), autoimmune disorders (e.g.
CC systemic lupus erythematosus and immune-related glomerulonephritis
CC rheumatoid arthritis), viral infections (e.g. herpes viruses, pox
CC viruses and adenoviruses), inflammation, graft vs host disease,
CC acute graft rejection and chronic graft rejection. Antagonists
CC can be used to treat diseases associated with increased apoptosis
CC including AIDS, neurodegenerative disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC retinitis pigmentosa, cerebellar degeneration), myelodysplastic
CC syndromes (e.g. aplastic anemia), ischemic injury (e.g. that
CC caused by myocardial infarction, stroke and reperfusion injury),
CC toxin-induced liver disease (e.g. that caused by alcohol), septic
CC shock, cachexia, anorexia, inflammatory diseases and stress response

CC related diseases, such as inflammatory bowel disease, rheumatoid
CC arthritis, osteoarthritis, psoriasis and septicemia. The products
CC can also be used for detection and diagnosis.

XX Sequence 655 AA;

Query Match 100.0%; Score 655; DB 20; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTTAQPEQKASNLIGTVRHVDRA 60

Db 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTTAQPEQKASNLIGTVRHVDRA 60

Qy 61 TGOVLTCDCPKAGTYVSEHCTNTSLRVCSSCPVCTFTRHENGIEKHCDCSCPCWPMTIEK 120

Db 61 TGOVLTCDCPKAGTYVSEHCTNTSLRVCSSCPVCTFTRHENGIEKHCDCSCPCWPMTIEK 120

Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVRKKGTETEDVRCCKQCARGTFSDVP 180

Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVRKKGTETEDVRCCKQCARGTFSDVP 180

Qy 181 SSVNKKAYTDCLSQNLVVIKPGTKETDNVCGTILPSFSSSTSPSPGTAIFPRPEHMETHE 240

Db 181 SSVNKKAYTDCLSQNLVVIKPGTKETDNVCGTILPSFSSSTSPSPGTAIFPRPEHMETHE 240

Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARGKEDVNTKLPNLQVNVH 300

Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARGKEDVNTKLPNLQVNVH 300

Qy 301 QQGPVHRRHILKLLPSMEATGGEKSTPIKGPGRHPRQNLKHFDINHLPMIVLFLLL 360

Db 301 QQGPVHRRHILKLLPSMEATGGEKSTPIKGPGRHPRQNLKHFDINHLPMIVLFLLL 360

Qy 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNKREKVIYCYNGHGIDILK 420

Db 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNKREKVIYCYNGHGIDILK 420

Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYADHERAYAAQLQHWITRGPEASLAQLIS 480

Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYADHERAYAAQLQHWITRGPEASLAQLIS 480

Qy 481 ALRQRRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPISPNKLENSALLTVPEP 540

Db 481 ALRQRRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPISPNKLENSALLTVPEP 540

Qy 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKDVLQVRLDPCDLQPIF 600

Db 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKDVLQVRLDPCDLQPIF 600

Qy 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKQSEASOTLLDSVYSHLPDLL 655

Db 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKQSEASOTLLDSVYSHLPDLL 655

RESULT 3

AAW81059

ID AAW81059 standard; Protein: 655 AA.

XX AC AAW81059;

DT 02-FEB-2001 (first entry)

XX Human tumour necrosis factor receptor TR9.

XX Human; tumour necrosis factor; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;

CC length gene may be used as hybridization probes for a cDNA library to
 CC isolate the full length gene and to isolate other genes which have a
 CC high sequence similarity. The probes may be used to identify a cDNA
 CC clone corresponding to a full length transcript and a genomic clone
 CC or clones that contain the complete gene including regulatory and
 CC promoter regions, exons, and introns.

XX
 SQ Sequence 655 AA;
 Query Match 100.0%; Score 655; DB 21; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGFLSTTTAAPEQKASNLIGTYRHVDRA 60
 Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGFLSTTTAAPEQKASNLIGTYRHVDRA 60
 Qy 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQPCPWPMEK 120
 Db 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQPCPWPMEK 120
 Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
 Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
 Qy 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPFSSTSPSGTAIPRPEHMETHE 240
 Db 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPFSSTSPSGTAIPRPEHMETHE 240
 Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
 Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
 Qy 301 QOGPHRHILKLLPSMEATGKESSTPIKGPGRHPRONLKHKFDINEHLPWMTVLFLLL 360
 Db 301 QOGPHRHILKLLPSMEATGKESSTPIKGPGRHPRONLKHKFDINEHLPWMTVLFLLL 360
 Qy 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMTPQNREKIYICNGHIGDILK 420
 Db 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMTPQNREKIYICNGHIGDILK 420
 Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 Qy 481 ALRQHRNDVVVEKIRGLMEDTQLETDKLALPMSPLSPSPSPNKLNSALLTVEP 540
 Db 481 ALRQHRNDVVVEKIRGLMEDTQLETDKLALPMSPLSPSPSPNKLNSALLTVEP 540
 Qy 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVLVLRQVRLDPCDLQPIF 600
 Db 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVLVLRQVRLDPCDLQPIF 600
 Qy 601 DDMHLFNLPELRVIEIPOAEDKLDRLFEIIGVKSQEASQTLDSVYSHLPDLL 655
 Db 601 DDMHLFNLPELRVIEIPOAEDKLDRLFEIIGVKSQEASQTLDSVYSHLPDLL 655

RESULT 5

AAB01338
 ID AAB01338 standard; Protein: 655 AA.
 XX
 AC AAB01338;
 XX
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE DR-6 death receptor.
 XX
 KW UL144; death receptor; apoptosis; programmed cell death; Fas;
 KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
 KW human.
 XX
 OS Homo sapiens.

XX WO2000034335-A2.
 XX
 PD 15-JUN-2000.
 XX 03-DEC-1999; 99WO-US26035.
 PF
 XX 04-DEC-1998; 98US-0205018.
 PR
 XX (SCHE) SCHERING CORP.
 PA
 XX Leong C, Phillips JH;
 PI
 XX WPI; 2000-423383/36.
 DR
 XX
 PT Purified or recombinant polypeptide for modulating apoptosis comprises
 a sequence which binds to an antibody specific for ULL144 or its
 fragments
 PT
 XX
 PS Disclosure; Page 68-70; 76pp; English.
 XX
 CC A pure or recombinant polypeptide which binds to a polyclonal antibody
 specific for the mature Ull144 is useful for screening molecules which
 CC block induction of apoptosis or interfere with antiapoptotic activity.
 CC The polypeptide is also useful for modulating apoptosis and useful in
 CC treatment of conditions associated with abnormal physiology or
 CC development, such as cancer or degenerative conditions and for
 CC regulation of viral infection and replication. At least five
 CC different death receptors are known, which include the CD95
 CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
 CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
 CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
 CC
 XX Sequence 655 AA;

Query Match 100.0%; Score 655; DB 21; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGFLSTTTAAPEQKASNLIGTYRHVDRA 60
 Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGFLSTTTAAPEQKASNLIGTYRHVDRA 60
 Qy 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQPCPWPMEK 120
 Db 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQPCPWPMEK 120
 Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
 Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
 Qy 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPFSSTSPSGTAIPRPEHMETHE 240
 Db 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPFSSTSPSGTAIPRPEHMETHE 240
 Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
 Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
 Qy 301 QOGPHRHILKLLPSMEATGKESSTPIKGPGRHPRONLKHKFDINEHLPWMTVLFLLL 360
 Db 301 QOGPHRHILKLLPSMEATGKESSTPIKGPGRHPRONLKHKFDINEHLPWMTVLFLLL 360
 Qy 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMTPQNREKIYICNGHIGDILK 420
 Db 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMTPQNREKIYICNGHIGDILK 420
 Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 Qy 481 ALRQHRNDVVVEKIRGLMEDTQLETDKLALPMSPLSPSPSPNKLNSALLTVEP 540
 Db 481 ALRQHRNDVVVEKIRGLMEDTQLETDKLALPMSPLSPSPSPNKLNSALLTVEP 540

Db 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPNAKLNSALLTVEP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITTEKKDVTLRQVRLDPCDQPIF 600
 Db 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITTEKKDVTLRQVRLDPCDQPIF 600
 QY 601 DMLHFLNPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLDSVYSHLPDLL 655
 Db 601 DMLHFLNPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLDSVYSHLPDLL 655

RESULT 6
 AAY77460
 ID AAY77460 standard; Protein: 655 AA.
 AC AAY77460;
 XX
 DT 05-JUN-2000 (first entry)
 XX Human TNF receptor-like protein HSLJD37R, SEQ ID NO:10.
 XX
 KW TNF receptor family; tumour necrosis factor; HDTEA84; HSLJD37R;
 KW Rank-like protein; RANKL; immune disorder; inflammation; allergy;
 KW immunosuppressant; antiarthritic; antirheumatoid; antiinflammatory;
 KW dermatological; antithyroid.
 XX
 OS Homo sapiens.
 XX
 XX W0200001817-A2.
 PN 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-US12366.
 XX
 PR 06-JUL-1998; 98US-0110938.
 PR 13-JUL-1998; 98US-0114466.
 PR 23-JUL-1998; 98US-0093897.
 PR 12-AUG-1998; 98US-0132968.
 PR 18-AUG-1998; 98US-0136214.
 PR 11-SEP-1998; 98US-0099999.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 XX Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, Gorman DM;
 PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
 PI Bazan JF, Mahony D, Lees EM;
 XX
 XX WPI: 2000-171015/15.
 DR N-PSDB; AA292406.
 XX
 XX New isolated mammalian genes, used to develop products for treating
 PT e.g. immune, inflammatory or allergic abnormalities, cancers or
 PT degenerative conditions
 XX
 PS Claim 24; Page 163-165; 218pp; English.

The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor) receptor family-related proteins HDTEA84, HSLJD37R and RANKL; human CC chemokine HCC5; human deubiquitinating proteins DUB1 and DUB12; human MD-1 and human and murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used to mediate uptake of substrates (e.g., prostaglandin-like molecules), to modulate or mediate cellular interactions (e.g., induce or prevent trafficking, proliferation, or differentiation of cells), or are intracellular proteins which are important in various cellular processes such as the deubiquitination of proteins or cell cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or allergic disorders, or abnormal cellular proliferation, for example,

CC cancers or degenerative conditions. They can be used to modulate immune responses in disease states e.g., autoimmune disorders, including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's thyroiditis, as well as acute and chronic inflammatory responses in which T cell activation, expansion, and/or immunological T cell memory play an important role. Sequences AAY77458-Y77461 and AAY77465-Y77468 represent TNF receptor family-related proteins. AAY77458 is the human protein HDTEA84, AAY77459-Y77461 are human HSLJD37R proteins, AAY77465 is murine Rank-like protein RANKL, and AAY77466-Y77468 are human RANKL proteins.

XX
 SQ Sequence 655 AA;
 Query Match 100.0%; Score 655; DB 21; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels. 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAAQPEQKASNLIGTYRHVDRA 60
 Db 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAAQPEQKASNLIGTYRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVSCSPVGTETRHENGIEKCHDCSQCPWPMIEK 120
 Db 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVSCSPVGTETRHENGIEKCHDCSQCPWPMIEK 120
 QY 121 LPCAALTDRRECTCPGCMFQSNATCAPHTVCPVGWGVKKGTEDEYRCKQARGTFSVDP 180
 Db 121 LPCAALTDRRECTCPGCMFQSNATCAPHTVCPVGWGVKKGTEDEYRCKQARGTFSVDP 180
 QY 181 SSVMKCKAYTDCLSQNLVVKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 Db 181 SSVMKCKAYTDCLSQNLVVKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSSASVPRPKVLSSTQEGTVPDNTSSARGKEDVANKTLNLOVNH 300
 Db 241 VPSSTYVPKGMNSTESNSSASVPRPKVLSSTQEGTVPDNTSSARGKEDVANKTLNLOVNH 300
 QY 301 QQGPHRHILKLLPSMEATGGEKSSSTPIKPKRGHPRQNLHKHFDINEHLPWMIVLFLLL 360
 Db 301 QQGPHRHILKLLPSMEATGGEKSSSTPIKPKRGHPRQNLHKHFDINEHLPWMIVLFLLL 360
 QY 361 VLVIIVVCSIRKSRRLKKGPRQDPSAIVEKAGLKKKSMPTONREKWIYCNHGHGIDILK 420
 Db 361 VLVIIVVCSIRKSRRLKKGPRQDPSAIVEKAGLKKKSMPTONREKWIYCNHGHGIDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSGNYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSGNYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPNAKLNSALLTVEP 540
 Db 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPNAKLNSALLTVEP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITTEKKDVTLRQVRLDPCDQPIF 600
 Db 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITTEKKDVTLRQVRLDPCDQPIF 600
 QY 601 DMLHFLNPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLDSVYSHLPDLL 655
 Db 601 DMLHFLNPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLDSVYSHLPDLL 655

RESULT 7
 AAU29232
 ID AAU29232 standard; Protein: 655 AA.
 XX
 XX AAU29232;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #209.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

XX 03-MAR-2000; 2000US-187202P.

XX 06-MAR-2000; 2000US-186968P.

XX 14-MAR-2000; 2000US-189320P.

XX 14-MAR-2000; 2000US-189328P.

XX 15-MAR-2000; 2000WO-US06884.

XX 21-MAR-2000; 2000US-190828P.

XX 21-MAR-2000; 2000US-191007P.

XX 21-MAR-2000; 2000US-191048P.

XX 21-MAR-2000; 2000US-191314P.

XX 28-MAR-2000; 2000US-192655P.

XX 29-MAR-2000; 2000US-193032P.

XX 29-MAR-2000; 2000US-193053P.

XX 30-MAR-2000; 2000WO-US08439.

XX 04-APR-2000; 2000US-194449P.

XX 04-APR-2000; 2000US-194647P.

XX 11-APR-2000; 2000US-195975P.

XX 11-APR-2000; 2000US-196000P.

XX 11-APR-2000; 2000US-196187P.

XX 11-APR-2000; 2000US-196690P.

XX 11-APR-2000; 2000US-196820P.

XX 18-APR-2000; 2000US-198121P.

XX 18-APR-2000; 2000US-198585P.

XX 25-APR-2000; 2000US-199397P.

XX 25-APR-2000; 2000US-199550P.

XX 25-APR-2000; 2000US-199654P.

XX 03-MAY-2000; 2000US-201516P.

XX 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

XX 30-MAY-2000; 2000WO-US14941.

XX 02-JUN-2000; 2000WO-US15264.

XX 05-JUN-2000; 2000US-209832P.

XX 28-JUL-2000; 2000WO-US20710.

XX 22-AUG-2000; 2000US-0644848.

XX 24-AUG-2000; 2000WO-US23328.

XX 08-NOV-2000; 2000WO-US30952.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000WO-US34956.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-602746/68.

XX N-PSDB; AAS46133.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the

XX presence of tumours, such as prostate and breast tumours, in mammals and

XX to screen for modulators of the compounds -

XX Claim 11; Fig 418; 774pp; English.

CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders.

XX SQ Sequence 655 AA;

Query Match 100.0%; Score 655; DB 22; Length 655;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTAQPQKASNLGTYRHVDRA 60

DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTAQPQKASNLGTYRHVDRA 60

QY 61 TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCSCPCWPMIEK 120

DB 61 TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCSCPCWPMIEK 120

QY 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVGRKKGTTETEDVRCCKCARGTFSVDP 180

DB 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVGRKKGTTETEDVRCCKCARGTFSVDP 180

QY 181 SSVMKCRAYTCLSONLVVVKPGTKETDNVCGTLPSSSSSTSPSGTAIFRPRHEMETH 240

DB 181 SSVMKCRAYTCLSONLVVVKPGTKETDNVCGTLPSSSSSTSPSGTAIFRPRHEMETH 240

QY 241 VPSSTYVPKGMNSTESSASVRPKVLSIOEGTVPDNTSSARKEDVNTKLPNLYVNH 300

DB 241 VPSSTYVPKGMNSTESSASVRPKVLSIOEGTVPDNTSSARKEDVNTKLPNLYVNH 300

QY 301 QGPHRRHILKLLPSMEATGGEKSTPIKPKRGHPRONLKHFDINEHLPMIYVLFLL 360

DB 301 QGPHRRHILKLLPSMEATGGEKSTPIKPKRGHPRONLKHFDINEHLPMIYVLFLL 360

QY 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKMTPTQNRKWTYYCNGHGIDILK 420

DB 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKMTPTQNRKWTYYCNGHGIDILK 420

QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAPSNYGTADHERAYAAALQHWITRGPEASLAQLIS 480

DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAPSNYGTADHERAYAAALQHWITRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTLQETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540

DB 481 ALRQHRNDVVEKIRGLMEDTTLQETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540

QY 541 SPQDKNGKFFVDESEPLLRCDSTSGSSALSRNGSFITKEKKDVTLRQVRLDPCDLP 600

DB 541 SPQDKNGKFFVDESEPLLRCDSTSGSSALSRNGSFITKEKKDVTLRQVRLDPCDLP 600

QY 601 DDLHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQSLDSDSVSHLPDLL 655

DB 601 DDLHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQSLDSDSVSHLPDLL 655

RESULT 8

AAE21958

ID AAE21958 standard; Protein; 655 AA.

XX AAE21958;

XX AC AAE21958;

XX 25-JUL-2002 (first entry)

XX Human death domain containing receptor (DR6) protein.

XX Human; therapy; death domain containing receptor; DR6; receptor; anaemia;

XX apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;

KW

KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
 KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
 KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
 KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;
 KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
 KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
 KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;
 KW dermatological; hepatotropic; antibacterial.
 XX
 OS Homo sapiens.

XX
 PH Key Location/Qualifiers
 FT Peptide 1..41
 FT /label= Signal_peptide
 FT Protein 41..655
 FT /note= "Mature human DR6"
 FT Domain 39..76
 FT /note= "TNFR cysteine rich domain"
 FT Domain 77..118
 FT /note= "TNFR cysteine rich domain"
 FT Domain 119..162
 FT /note= "TNFR cysteine rich domain"
 FT Domain 163..201
 FT /note= "TNFR cysteine rich domain"
 FT Domain 339..351
 FT /note= "Transmembrane domain"
 FT Domain 360..370
 FT /note= "Transmembrane domain"

WO200185209-A2.

15-NOV-2001.

30-APR-2001; 2001WO-US11735.

10-MAY-2000; 2000US-203015P.

(ELIL) LILLY & CO ELI.

Heuer JG, Liu J, Na S, Song HY, Yang D;

WPI; 2002-351283/38.

N-PSDB; AAD35053.

XX Treating or preventing T cell or Th2 cell mediated condition e.g.,
 XX asthma or multiple sclerosis in mammal, comprises administering
 XX composition comprising death domain containing receptor, DR6 agonist or
 XX antagonist -

PS Claim 11; Page 126-129; 133pp; English.

XX The invention relates to a method for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. The
 CC method comprising administering to the mammal a pharmaceutical
 CC composition comprising a death domain containing receptor (DR6) agonist
 CC or antagonist. The method is useful for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6
 CC agonist is useful in the manufacture of a medicament for treating or
 CC preventing at least one symptom associated with aberrant apoptosis.
 CC graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma,
 CC atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
 CC insulin-dependent diabetes mellitus, cancer, multiple sclerosis,
 CC Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic
 CC lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
 CC autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing
 CC lung disease, organ rejection after transplantation, thrombotic
 CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
 CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
 CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
 CC for treating or preventing at least one symptom associated with
 CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial

CC infection, complications of infection, human immunodeficiency virus
 CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
 CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
 CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
 CC associated ulceration, cytoprotection during cancer treatment,
 CC recuperation from chemotherapy, recuperation from irradiation therapy,
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. The present sequence is human DR6 protein.
 XX
 SQ Sequence 655 AA;

Query Match 100.0%; Score 655; DB 23; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSALASCRIARRATATMTAGSLLGLLSTTTTAQPEQKASNLIGTYRHVDRA 60
 DB 1 MGTSPSSSALASCRIARRATATMTAGSLLGLLSTTTTAQPEQKASNLIGTYRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVTGTRHENGIEKCHDCSQPCPWPWIEK 120
 DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVTGTRHENGIEKCHDCSQPCPWPWIEK 120
 QY 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPGCGVGRKKGTETEDVRCKQCARGTSDVP 180
 DB 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPGCGVGRKKGTETEDVRCKQCARGTSDVP 180
 QY 181 SSVMKCKAYTDCLSQNLVVKPCTKTDNVCGTLPFSFSSSTSPSPCTAIFPRPEHMETHE 240
 DB 181 SSVMKCKAYTDCLSQNLVVKPCTKTDNVCGTLPFSFSSSTSPSPCTAIFPRPEHMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSTQCTGTPDNTSSARGKEDVANKTLPNLQVNH 300
 DB 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSTQCTGTPDNTSSARGKEDVANKTLPNLQVNH 300
 QY 301 QOGPHRHILKLLPSMEATGGEKSSPTPIKGRKGRHPRQNLKHFDINEHLPWMLVFLLL 360
 DB 301 QOGPHRHILKLLPSMEATGGEKSSPTPIKGRKGRHPRQNLKHFDINEHLPWMLVFLLL 360
 QY 361 VLWVIWVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTONREKWIYCNCHGDIILK 420
 DB 361 VLWVIWVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTONREKWIYCNCHGDIILK 420
 QY 421 LVAAQVGSQWKDIQFLCNASEREVAAFSNGYTADHERAYAAALQHWITIRGPASLAQLIS 480
 DB 421 LVAAQVGSQWKDIQFLCNASEREVAAFSNGYTADHERAYAAALQHWITIRGPASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRRNGSFTITKEKDDTVLRQVRLDPCDQPIF 600
 DB 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRRNGSFTITKEKDDTVLRQVRLDPCDQPIF 600
 QY 601 DDMHLFNLPEELRVEEIPQAEKDLRLFEIIGVKVSQEAASQTLDSVYSHLPDLL 655
 DB 601 DDMHLFNLPEELRVEEIPQAEKDLRLFEIIGVKVSQEAASQTLDSVYSHLPDLL 655

RESULT 9

AA92846

ID AAY92846 standard; Protein; 691 AA.

XX AC AAY92846;

XX DT 29-AUG-2000 (first entry)

XX DE Human osteoprotegrin-like 4 (OPGx4) protein.

XX KW OPGx4; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;

KW inhibitor; bone resorption; vascular calcification; apoptosis;

KW osteopathic.

CC lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
CC autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing
CC lung disease, organ rejection after transplantation, thrombotic
CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
CC for treating or preventing at least one symptom associated with
CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
CC infection, complications of infection, human immunodeficiency virus
CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
CC associated ulceration, cytoprotection during cancer treatment,
CC recuperation from chemotherapy, recuperation from irradiation therapy,
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. The present sequence is human DR6 protein fragment.

XX Sequence 631 AA;

Query Match 96.3%; Score 631; DB 23; Length 631;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 MIAGSLLLGLFSTTTAQPEQKASNLIGTYRHVDRATQVLTCDKCPAGTYVSEHCTNTS 84
DB 1 MIAGSLLLGLFSTTTAQPEQKASNLIGTYRHVDRATQVLTCDKCPAGTYVSEHCTNTS 60
QY 85 LRVSSCPVGFTRHENGIEKHCHDCSQPCPMPMEIKLPCAAALTDRECTCPGPMFQSNATC 144
DB 61 LRVSSCPVGFTRHENGIEKHCHDCSQPCPMPMEIKLPCAAALTDRECTCPGPMFQSNATC 120
QY 145 APHTVCPVGVGRKGTETEDVRCKQARGTFSDVPSSVMCKAYTDCLSQNLVYIKPGT 204
DB 121 APHTVCPVGVGRKGTETEDVRCKQARGTFSDVPSSVMCKAYTDCLSQNLVYIKPGT 180
QY 205 KETDNVCGTLPSFSSSTSPGTAIFPRPEHMETHEVPSSTYVVPKGMNSTESNSSASVRP 264
DB 181 KETDNVCGTLPSFSSSTSPGTAIFPRPEHMETHEVPSSTYVVPKGMNSTESNSSASVRP 240
QY 265 KYLSIQGTVPDNTSSARGEDVNKTLPNLQVNVHQGPQPHRHILKLLPSMEATGGEKS 324
DB 241 KYLSIQGTVPDNTSSARGEDVNKTLPNLQVNVHQGPQPHRHILKLLPSMEATGGEKS 300
QY 325 STPIKPRGRHPRQNLKHFEDINEHLPWMIIVLFLLLVLIIVVCSIRKSSRTLKKGPRQD 384
DB 301 STPIKPRGRHPRQNLKHFEDINEHLPWMIIVLFLLLVLIIVVCSIRKSSRTLKKGPRQD 360
QY 385 PSAIVEKAGLKKSMPTTONREKWIYCYNGHGDIDILKLVAAQVGSQWKDIYQFLCNASERE 444
DB 361 PSAIVEKAGLKKSMPTTONREKWIYCYNGHGDIDILKLVAAQVGSQWKDIYQFLCNASERE 420
QY 445 VAAFSNGYTAHERAYALQHWITIRGPASLAQLISALRQHRNDVVEKIRGLMEDTTQL 504
DB 421 VAAFSNGYTAHERAYALQHWITIRGPASLAQLISALRQHRNDVVEKIRGLMEDTTQL 480
QY 505 ETDKALPMSPLSPSPISPNAKLENSALLITVPSQDNKNGFFVDESEPLLCDSTS 564
DB 481 ETDKALPMSPLSPSPISPNAKLENSALLITVPSQDNKNGFFVDESEPLLCDSTS 540
QY 565 SGSSALSRLNGSPFITREKDKTVLRQVRLDPDQLQPIFDDMLHFLNPEELRVEEIPQAEK 624
DB 541 SGSSALSRLNGSPFITREKDKTVLRQVRLDPDQLQPIFDDMLHFLNPEELRVEEIPQAEK 600
QY 625 LDRLEFIIGVKSQEASQTLDSVYSHLPDLL 655
DB 601 LDRLEFIIGVKSQEASQTLDSVYSHLPDLL 631

RESULT 12

AAW75792

ID AAW75792 standard; Protein; 655 AA.

XX AAW75792;
AC 21-DEC-1998 (first entry)
DE Human tumour necrosis factor related receptor TR7.
KW Tumour necrosis factor related receptor; TR7; human; inflammation;
KW arthritis; septicaemia; autoimmune disease; psoriasis;
KW inflammatory bowel disease; infection; graft-versus-host disease;
KW transplant rejection; stroke; acute respiratory disease syndrome;
KW ischaemia; restenosis; brain injury; AIDS; bone disease; cancer;
KW atherosclerosis; Alzheimer's disease; diagnosis; therapy; vaccine.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 24 /note= "encoded by ACG"
FT XX
PN EP869179-A1.
XX
PD 07-OCT-1998.
XX
PF 01-APR-1998; 98EP-0302528.
XX
PR 28-OCT-1997; 97US-0959382.
PR 02-APR-1997; 97US-0041796.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Hurle MR, Tan KB, Young P;
XX
DR WPI: 1998-508493/44.
DR N-PSDB; AAV57441.
XX
PT New tumour necrosis factor receptor TR7 polypeptides and
PT polynucleotides - useful as diagnostic reagents and for treating
PT Alzheimer's disease, AIDS and cancer
XX
PS Claim 11; Page 19-21; 25pp; English.
XX
CC This is the amino acid sequence of a novel member of the human
CC tumour necrosis factor (TNF) receptor superfamily, termed TR7.
CC It was deduced from the coding regions of overlapping isolated
CC cDNA clones (see AAV57441). Expression systems, host cells and a
CC method of producing TR7 polypeptides are claimed. TR7 polypeptides
CC are useful for diagnosing diseases or susceptibility to diseases by
CC determining TR7 polypeptide or mRNA expression. TR7 polypeptide
CC can be used to screen for agonists and antagonists which bind the
CC receptor. These can be used in treatment to inhibit or enhance TR7
CC activity. TR7 antibodies are generated using TR7 polypeptide
CC fragments, and are used for treatment of diseases. TR7 polypeptides
CC and polynucleotides can be administered directly as vaccines for
CC prevention of diseases. Diseases diagnosed, treated or prevented
CC by the above methods include: chronic and acute inflammation,
CC arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel
CC disease, psoriasis), transplant rejection, graft vs. host disease,
CC infection, stroke, ischaemia, acute respiratory disease syndrome,
CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
CC lymphoproliferative disorders), atherosclerosis, and Alzheimer's
CC disease.
XX
SQ Sequence 655 AA;

Query Match 96.3%; Score 631; DB 19; Length 655;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 MIAGSLLLGLFSTTTAQPEQKASNLIGTYRHVDRATQVLTCDKCPAGTYVSEHCTNTS 84

DB 25 MIAGSLLLGLFSTTTAQPEQKASNLIGTYRHVDRATQVLTCDKCPAGTYVSEHCTNTS 84


```

QY 85 LRVCCSPVGTTRHENGIEKCHDCSQCPWPMIEKLPAAALTDRECTCPGPMFQSNATC 144
Db 85 LRVCCSPVGTTRHENGIEKCHDCSQCPWPMIEKLPAAALTDRECTCPGPMFQSNATC 144
QY 145 APHTVCPVGVGVRKKGTEDEVRCKQCARGTFSVPSSVMKCKATDCLSNLYVIRPQT 204
Db 145 APHTVCPVGVGVRKKGTEDEVRCKQCARGTFSVPSSVMKCKATDCLSNLYVIRPQT 204
QY 205 KETDNVCGTLPSFSSTSPSGTAIFPRPEHMETHEVPSSYVVPKGMNSTESNSASVYP 264
Db 205 KETDNVCGTLPSFSSTSPSGTAIFPRPEHMETHEVPSSYVVPKGMNSTESNSASVYP 264
QY 265 KVLSSIQEGTVPDNTSSARGEDVKNLPLNQVYVHQQGPHRHILKLLPSMEATGGEKS 324
Db 265 KVLSSIQEGTVPDNTSSARGEDVKNLPLNQVYVHQQGPHRHILKLLPSMEATGGEKS 324
QY 325 STPIKGRKGRHPRQNLHKHFDINEHLPMMIVLFLLLVLVTVVCSIRKSSRTLKKGPRQD 384
Db 325 STPIKGRKGRHPRQNLHKHFDINEHLPMMIVLFLLLVLVTVVCSIRKSSRTLKKGPRQD 384
QY 385 PSAIVEKAGLKSMPTQNTREKWTYYCNGHGIDILKLVAAQVGSQWKDIYQFLCNASERE 444
Db 385 PSAIVEKAGLKSMPTQNTREKWTYYCNGHGIDILKLVAAQVGSQWKDIYQFLCNASERE 444
QY 445 VAFSNGYTADHERAYAAALQHTVIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTQOL 504
Db 445 VAFSNGYTADHERAYAAALQHTVIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTQOL 504
QY 505 ETDKLALPMSPLSPSPSPNAKLENSALLTVPEPSQDNKNGFFVDESEPLLRCDSTS 564
Db 505 ETDKLALPMSPLSPSPSPNAKLENSALLTVPEPSQDNKNGFFVDESEPLLRCDSTS 564
QY 565 SGSSALSRNGSFTKEKKDVLROVRDPCDQLQIFDDMLHFLNPEELRVIEEIPQAEK 624
Db 565 SGSSALSRNGSFTKEKKDVLROVRDPCDQLQIFDDMLHFLNPEELRVIEEIPQAEK 624
QY 625 LDRLEFIIGVKSQASOTLLDSVYSHLPDLL 655
Db 625 LDRLEFIIGVKSQASOTLLDSVYSHLPDLL 655

```

RESULT 13

AAB44249

ID AAB44249 standard; Protein; 655 AA.

AC AAB44249;

XX

DT 08-FEB-2001 (first entry)

XX Human PR0868 (UNQ437) protein sequence SEQ ID NO:64.

DE Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;

XX expressed sequence tag; detection; cancer.

KW Homo sapiens.

XX W0200053756-A2.

XX 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US04341.

XX 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 21-APR-1999; 99US-0126773.

PR 28-APR-1999; 99US-0130232.

PR 14-MAY-1999; 99US-0131445.

PR 23-JUN-1999; 99US-0134287.

PR 28-JUL-1999; 99US-0141037.

PR 30-OCT-1999; 99US-0145698.

PR 02-DEC-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

XX (GETH) GENENTECH INC.

XX PA

XX ASKenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;

PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WJ;

XX WPI; 2000-611443/58.

DR N-PSDB; AAC78474.

XX Novel PRO polypeptides and polynucleotides used in detection methods,

PT to target bioactive molecules to specific cells, and to modulate

PT cellular activities

XX Claim 12; Fig 26; 636pp; English.

PS AAC78458 to AAC78599 represent polynucleotide and EST (expressed

XX sequence tag) sequences which encode secreted or transmembrane PRO

CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic

CC activity. The polynucleotides and polypeptides can be used for detecting

CC the presence of PRO polypeptides in samples, for linking bioactive

CC molecules to cells and for modulating biological activities of cells,

CC using the polypeptides for specific targeting. The polypeptide targeting

CC can be used to kill the target cells, e.g. for the treatment of cancers.

CC The polypeptide pairs provide specific targeting of bioactive molecules

CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in

CC the isolation of the PRO polynucleotide sequences.

XX SQ Sequence 655 AA;

Query Match 84.6%; Score 554; DB 21; Length 655;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFTTTAAQPEQKASNLIGTYRHVDRA 60

Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFTTTAAQPEQKASNLIGTYRHVDRA 60

QY 61 TGQVLTCDKCPAGTYVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQCPWPMIEK 120

Db 61 TGQVLTCDKCPAGTYVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQCPWPMIEK 120

QY 121 LPCAALTDRECTCPGPMFQSNATCAPHTVCPGVGVRKKGTEDEVRCKOCARGTFSQVDP 180

Db 121 LPCAALTDRECTCPGPMFQSNATCAPHTVCPGVGVRKKGTEDEVRCKOCARGTFSQVDP 180

QY 181 SSVKCKAYTDCLSQNLVWIKPCTKEDNVCGTLPSFSSTSPSGTAIFPRPEHMETHE 240

Db 181 SSVKCKAYTDCLSQNLVWIKPCTKEDNVCGTLPSFSSTSPSGTAIFPRPEHMETHE 240

QY 241 VPSSTYVPGMNSTESNSASVPRKVLSSIQEGTVPDNTSSARGEDVKNLPLNQVYVH 300

Db 241 VPSSTYVPGMNSTESNSASVPRKVLSSIQEGTVPDNTSSARGEDVKNLPLNQVYVH 300

QY 301 QQGPVHRRHILKLLPSMEATGGEKSSYPIKGPGRHPRQNLHKHFDINEHLPMMIVLFLLL 360

Db 301 QQGPVHRRHILKLLPSMEATGGEKSSYPIKGPGRHPRQNLHKHFDINEHLPMMIVLFLLL 360

QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNTREKWTYYCNGHGIDILK 420

Db 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNTREKWTYYCNGHGIDILK 420

QY 421 LVAAQVGSQWKDIYQFLCNASEREVAFNSGYTADHERAYAAALQHTVIRGPEASLAQLIS 480

Db 421 LVAAQVGSQWKDIYQFLCNASEREVAFNSGYTADHERAYAAALQHTVIRGPEASLAQLIS 480

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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:50:18 ; Search time 15 seconds
(without alignments)
1811.133 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTPSPSSTALASCSRIARR.....SQEASQTLDSVYSHLPDLL 655

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	655	1	TR21_HUMAN
2	111	16.9	655	1	TR21_MOUSE
3	8	1.2	180	1	HM12_CAEEL
4	8	1.2	407	1	YAE1_SCHPO
5	8	1.2	503	1	Y21_Hpv21
6	8	1.2	507	1	YG46_YEAST
7	8	1.2	555	1	GP1_CHLRE
8	8	1.2	806	1	TRAL_MAIZE
9	8	1.2	987	1	EPB4_HUMAN
10	8	1.2	1251	1	YQ03_CAEEL
11	7	1.1	129	1	YVBH_BAGSU
12	7	1.1	135	1	INL5_MOUSE
13	7	1.1	161	1	19KD_MYCAV
14	7	1.1	178	1	X319_MYCGE
15	7	1.1	188	1	DSBE_YERPE
16	7	1.1	194	1	TDX_FASHE
17	7	1.1	198	1	Y111_ROTBV
18	7	1.1	207	1	UB6B_MOUSE
19	7	1.1	223	1	NK12_MOUSE
20	7	1.1	227	1	RISB_ARATH
21	7	1.1	231	1	SGBE_HAEIN
22	7	1.1	245	1	MCT1_SHEEP
23	7	1.1	251	1	CRB1_HUMAN
24	7	1.1	251	1	MCT3_SHEEP
25	7	1.1	253	1	C1QB_MOUSE
26	7	1.1	266	1	BLO7_ECOLI
27	7	1.1	270	1	YB62_MYCPN
28	7	1.1	303	1	MURB_BAGSU
29	7	1.1	311	1	CC23_TRYBB
30	7	1.1	348	1	YX99_MYCTU
31	7	1.1	357	1	MYCM_HUMAN
32	7	1.1	360	1	UX0A_THEME
33	7	1.1	369	1	YS19_CAEEL

RESULT 1

ID	TR21_HUMAN	STANDARD	PRT	655 AA
AC	O75509	O96D86		
DT	15-JUN-2002	(Rel. 41, Created)		
DT	15-JUN-2002	(Rel. 41, Last sequence update)		
DE	Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-related death receptor-6) (Death receptor 6).			
GN	TNFRSF21 OR DR6			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98378343; PubMed=9714541;			
RA	Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.;			
RT	"Identification and functional characterization of DR6, a novel death domain-containing TNF receptor."			
RL	FEBS Lett. 431:351-356(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Parker A.;			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBSJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Colon;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.			
CC	-!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.			
CC	-!- SUBUNIT: Associates with TRADD.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).			
CC	-!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.			
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.			
CC	-----			
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CC	-----			
DR	EMBL; AF068868; AAC34583.1; -			
DR	EMBL; AL096801; CAB75692.1; -			
DR	EMBL; BC017730; AAH17730.1; -			
DR	EMBL; BC10241; AAH10241.1; ALT_INIT.			
DR	Genew; HGNC:13469; TNFRSF21.			

```

DR MW: 605732;
DR HSP: O14763; 1D0G.
DR InterPro: IPR000488; Death.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT DOMAIN 42 349
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 50 88
FT REPEAT 90 131
FT REPEAT 133 167
FT REPEAT 170 211
FT DISULFID 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
FT CARBOHYD 82 82
FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 278
FT CARBOHYD 289 289
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 100.0%; Score 655; DB 1; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATMTAGSLLGLFLSTTTTAQPEQKASNLGTYRHVDRA 60
DB 1 MGTSPSSSTALASCSRIARRATMTAGSLLGLFLSTTTTAQPEQKASNLGTYRHVDRA 60

QY 61 TGOVLTCDKCPAGTVVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQCPWPMEIK 120
DB 61 TGOVLTCDKCPAGTVVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQCPWPMEIK 120

QY 121 LFCALTDRETCPCPGMFOGNSATCAPHTVCPGVGWVKKGTETEDVRCKQCARGTSDVP 180
DB 121 LFCALTDRETCPCPGMFOGNSATCAPHTVCPGVGWVKKGTETEDVRCKQCARGTSDVP 180

QY 181 SSVMKCKAYTDCLSQNLVYIKGTETDNVCGTLPFSFSSSTSPSGCTAIFRPEHMETHE 240
DB 181 SSVMKCKAYTDCLSQNLVYIKGTETDNVCGTLPFSFSSSTSPSGCTAIFRPEHMETHE 240

QY 241 VPSSTVYVPGMNSTESNSASVRPKVLSSIQEGTVDPDNTSSARGKEDVNKTLPNLQVNVH 300
DB 241 VPSSTVYVPGMNSTESNSASVRPKVLSSIQEGTVDPDNTSSARGKEDVNKTLPNLQVNVH 300

QY 301 QOGPHRHRLTKLLPSNEATGGKSSPTPKGPRGRHQRNLNHFHFDINEHLPWMIVLFLLL 360
DB 301 QOGPHRHRLTKLLPSNEATGGKSSPTPKGPRGRHQRNLNHFHFDINEHLPWMIVLFLLL 360

QY 361 VLWVIWVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTPTONREKWIYCNHGHDILK 420
DB 361 VLWVIWVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTPTONREKWIYCNHGHDILK 420

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QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540

QY 541 SPQDKNGFFVDESEPLLCDDSTSSGSSALSRLNGSFITTEKKDKTVLRQVRLDPCDLPQIF 600
DB 541 SPQDKNGFFVDESEPLLCDDSTSSGSSALSRLNGSFITTEKKDKTVLRQVRLDPCDLPQIF 600

QY 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLDSVYSHLPDLL 655
DB 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLDSVYSHLPDLL 655

RESULT 2
TR21_MOUSE STANDARD; PRT; 655 AA.
AC Q9EP05: Q9LXH9; Q91W77;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
(RD6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT "Murine DR6: murine TNFR-related death receptor-6.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RC FUNCTION.
RX MEDLINE=21571606; PubMed=11714751;
RA Zhao H., Yan H., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal kinase activity and T cell
differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448(2001).
CC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
similarity). May activate JNK and be involved in T-cell
differentiation.
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC -!- May be involved in T-cell differentiation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
thymus, testis, prostate, ovary, small intestine, colon, brain,
lung and kidney, and in fetal brain, liver and lung. Detected at
lower levels in adult peripheral blood leukocytes, lung, and in
fetal muscle, heart, kidney, small intestine and skin. Detected in
T-cells, B-cells and monocytes. In T-cells expression is highest
in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.

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CC -----
DR EMBL; AF322069; AAG38115.1; -
DR EMBL; AY043489; AAK74193.1; -
DR EMBL; BC016420; AAHL6420.1; -
DR HSSP; O14763; IDOG.
DR MGD; MGI:2151075; Tnfrsf21.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT FT 42 655
FT FT 42 655
FT DOMAIN 42 349
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 90 88
FT REPEAT 133 167
FT REPEAT 170 211
FT DISULFID 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
FT DISULFID 192 211
FT CARBOHYD 82 82
FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 278
FT CARBOHYD 289 289
FT CONFLICT 352 352
FT CONFLICT 523 523
SQ SEQUENCE 655 AA; 71982 MW; 5EC7C51C7C99EFF7 CRC64;

Query Match 16.9%; Score 111; DB 1; Length 655;
Best Local Similarity 100.0%; Pred. No. 1.9e-102;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 NGHGTDLKLVAAQVGSQWKDIYQFLCNASREVAFAFNGYTAHERAYAAALQHWITRGP 471
DB 412 NGHGTDLKLVAAQVGSQWKDIYQFLCNASREVAFAFNGYTAHERAYAAALQHWITRGP 471

QY 472 EASLAQLISALRHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSP 522
DB 472 EASLAQLISALRHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSP 522

RESULT 3
ID HM12 CAEEL STANDARD; PRT; 180 AA.
AC P17487; Q9TZZ7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

```

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein ceh-12.
GN CEH-12 OR F33D11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Sammons L., Wohlmann P., Mullen G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 154-180 FROM N.A.
RX MEDLINE=90245646; PubMed=1970877;
RA Schaller D., Wittmann C., Spicher A., Mueller F., Tobler H.;
RT "Cloning and analysis of three new homeobox genes from the nematode
RT Caenorhabditis elegans";
RL Nucleic Acids Res. 18:2033-2036(1990).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -----
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CC -----
DR EMBL; AF039720; AAB96698.1; -
DR EMBL; X17076; CAA34928.1; -
DR PIR; S09504; S09504.
DR WormPep; F33D11.4; CE09894.
DR HSSP; P02836; IENH.
DR TRANSFAC; T02987; -
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_repressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT DNA_BIND 110 169
FT SEQUENCE 180 AA; 20296 MW; FC2117756F8D4376 CRC64;

Query Match 1.2%; Score 8; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 SFSSSTSP 223
DB 63 SFSSSTSP 70

RESULT 4
ID YAE1 SCHPO STANDARD; PRT; 407 AA.
AC Q09842;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C23D3.01 in chromosome I.
GN SPAC23D3.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

```

OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Delius H.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 DR EMBL; U31779; AAA79397.1; -
 DR HSSP; P03122; 2BOP.
 DR InterPro; IPR000427; E2_C.
 DR InterPro; IPR001866; E2_N.
 DR Pfam; PF00508; E2_N; 1.
 DR Pfam; PF00511; E2_C; 1.
 DR ProDom; PD000672; E2_C; 1.
 DR ProDom; PD000678; E2_N; 1.
 DR PROBLEM; PD000678; E2_N; 1.
 SQ SEQUENCE 503 AA; 56750 MW; AE72A9DF6367266 CRC64;

 QY Query Match 1.2%; Score 8; DB 1; Length 503;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 218 SSSTSPSP 225
 |||||
 Db 367 SSSTSPSP 374

 RESULT 6
 YG46_YEAST
 ID YG46_YEAST STANDARD; PRT; 507 AA.
 AC P53301;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 52.8 kDa protein in BUB1-H1P1 intergenic region.
 GN YGR189C OR G7553.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=97279231; PubMed=9133739;
 RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
 RA Nombela C.;
 RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm
 RT of Saccharomyces cerevisiae chromosome VII.";
 RL Yeast 13:357-363(1997).
 CC -!- SIMILARITY: SOME, TO YEAST UTR2.
 CC -----
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 CC -----
 DR EMBL; Z72974; CAA97215.1; -
 DR EMBL; X99074; CAA67525.1; -
 DR HSSP; P23904; 1AJK.
 DR SGD; S0003421; CRH1.
 DR InterPro; IPR000757; Glyco_hydro_16.
 DR Pfam; PF00722; Glyco_hydro_16; 1.
 KW Hypothetical protein.
 FT DOMAIN 63 66 POLY-SPR.


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FT DOMAIN 301 310 POLY-SER.
FT DOMAIN 345 357 POLY-SER.
FT DOMAIN 387 391 POLY-SER.
FT DOMAIN 467 470 POLY-SER.
SQ SEQUENCE 507 AA; 52757 MW; 7D7B61F57AEA942C CRC64;

Query Match 1.2%; Score 8; DB 1; Length 507;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10
DB 356 TSPSSSTA 363

RESULT 7
GPI_CHLRE STANDARD; PRT; 555 AA.
AC Q9FPQ6; Q03927;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
glycoprotein 1).
GN GPI.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21159092; PubMed=11258910;
RA Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
RA Goodenough U.W.;
RT "Glycosylated prolipoline II rods-with-kinks as a structural motif in
plant hydroxyproline-rich glycoproteins.";
RL Biochemistry 40:2978-2987(2001).
RN [2]
RP PARTIAL PRELIMINARY SEQUENCE FROM N.A.
RX MEDLINE=91017504; PubMed=1699225;
RA Adair W.S., Apt K.E.;
RT "Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
encoding cell wall hydroxyproline-rich glycoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
CC -!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
layer.
CC -!- SUBUNIT: Associates with GP2 and GP3.
CC -!- PTM: N-glycosylated and O-glycosylated.
CC
CC
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CC
CC EMBL; AF309494; AAG45420.1; -.
CC EMBL; M58496; AAG69706.1; ALT_SEQ.
CC GlycoSuiteDB; Q9FPQ6; -.
CC InterPro; IPR002965; P-rich_extensin.
CC PRINTS; IPR003882; Pistill_extensin.
CC PRINTS; PR01217; PRICHEXTENSIN.
CC PRINTS; PR01218; PSTLEXTENSIN.
CC Glycoprotein; Repeat; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 555 VEGETATIVE CELL WALL PROTEIN GPI.
FT DOMAIN 40 339 49 X 5 AA APPROXIMATE PPSXP REPEATS.
FT DOMAIN 259 279 POLY-PRO.
FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 555 AA; 54219 MW; 6A584A90465502F5 CRC64;
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Query Match 1.2%; Score 8; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 SPSPIPPSP 526
DB 366 SPSPIPPSP 373

RESULT 8
TRAIL_MAIZE STANDARD; PRT; 806 AA.
AC P08770;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Putative AC transposase (ORFA).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunze R., Stochaj U., Laufs J., Starling P.;
RT "Transcription of transposable element Activator (Ac) of Zea mays L.";
RL EMBO J. 6:1555-1563(1987).
CC -!- MISCELLANEOUS: THIS PROTEIN IS CODED BY THE TRANSPOSABLE MAIZE
CONTROLLING ELEMENT "ACTIVATOR" (AC), WHICH IS ABLE TO ACTIVATE
CHROMOSOME BREAKAGE AT A SPECIFIC LOCATION; IT MAY BE THE
STRUCTURAL GENE FOR A TRANS-ACTING FUNCTION REQUIRED FOR
TRANSPOSITION.
CC
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CC
CC EMBL; X05424; CAA29005.1; -.
CC MaizEDB; 65747; -.
CC InterPro; IPR003656; BED_finger.
CC Pfam; PF02892; zf-BED; 1.
CC Transposable element; Transposition; DNA-binding; DNA recombination;
KW Repeat.
FT INIT_MET 0
FT DOMAIN 108 127 10 X 2 AA TANDEM REPEATS OF P-[QE].
SQ SEQUENCE 806 AA; 91890 MW; B3B2B5BE79D53DED CRC64;

Query Match 1.2%; Score 8; DB 1; Length 806;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10
DB 68 TSPSSSTA 75

RESULT 9
EPB4_HUMAN STANDARD; PRT; 987 AA.
AC P54760; Q9BXPO; Q9BTA5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-B receptor 4 precursor (EC 2.7.1.112) (Tyrosine-protein
kinase receptor HTK).
GN EPB4 OR HTK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94245746; PubMed=8188704;
 RP Bennett B.D., Wang Z., Kuang W.J., Wang A., Groopman J.E.,
 RA Goeddel D.V., Scadden D.T.;
 RA "Cloning and characterization of HTK, a novel transmembrane tyrosine
 RT kinase of the Eph subfamily";
 RL J. Biol. Chem. 269:14211-14218(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RA "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [3]
 RN SEQUENCE OF 143-987 FROM N.A.
 RP TISSUE=Pancreas;
 RC Strausberg R.;
 RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RL
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
 CC EPHRIN-B2. MAY HAVE A ROLE IN EVENTS MEDIATING DIFFERENTIATION AND
 CC DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PLACENTA AND IN A
 CC RANGE OF PRIMARY TISSUES AND MALIGNANT CELL LINES. EXPRESSED IN
 CC FETAL, BUT NOT ADULT, BRAIN, AND IN PRIMITIVE AND MYELOID, BUT NOT
 CC LYMPHOID, HEMATOPOIETIC CELLS.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
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 CC
 DR EMBL; U07695; AAA20598.1; -;
 DR EMBL; AF312032; AAK21010.1; -;
 DR EMBL; BC004264; AAH04264.1; -;
 DR HSSP; P29323; 1B4F.
 DR Genew; HGNC:3395; EPHB4.
 DR MTM; 600011; -;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FN_III_repeat.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR Pfam; PF01404; EPH_lbd; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PROSITE; PS00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.

DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 987 EPHRIN TYPE-B RECEPTOR 4.
 FT DOMAIN 16 539 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 540 560 POTENTIAL.
 FT DOMAIN 561 987 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 184 320 CYS-RICH.
 FT DOMAIN 321 429 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 430 528 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 615 899 PROTEIN KINASE.
 FT DOMAIN 907 971 SAM.
 FT SITE 985 987 PD2-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 621 629 ATP (BY SIMILARITY).
 FT BINDING 647 647 ATP (BY SIMILARITY).
 FT ACT_SITE 740 740 BY SIMILARITY.
 FT MOD_RES 590 590 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 774 774 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 924 924 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 426 426 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 62 62 D -> E (IN REF. 1).
 FT CONFLICT 308 308 Y -> D (IN REF. 1).
 FT CONFLICT 464 464 V -> W (IN REF. 1).
 FT CONFLICT 926 927 ES -> AR (IN REF. 1).
 SQ SEQUENCE 987 AA; 108269 MW; 11A004622F194706 CRC64;
 Query Match 1.2%; Score 8; DB 1; Length 987;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 360 LVLWIVV 367
 Db 551 LVLWIVV 558
 RESULT 10
 YQY3_CABEL
 ID YQY3_CABEL STANDARD; PRT; 1251 AA.
 AC Q09550;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Hypothetical 133.5 kDa protein F26C11.3 in chromosome II.
 GN F26C11.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Matthews P.;
 RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Z47072; CAA87369.1;
DR WomPep; F26C11.3; CE01561.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 1.
DR SMART; SM00032; CCP; 1.
KW Hypothetical protein.
FT DOMAIN 120 414
SQ SEQUENCE 1251 AA; 133498 MW; 2B959ECA03B9954A CRC64;

Query Match 1.2%; Score 8; DB 1; Length 1251;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10
DB 850 TSPSSSTA 857
|||||||

RESULT 11
ID YVBH_BACSU STANDARD; PRT; 129 AA.
AC P37496;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yybh.
GN YVBH.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serior P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenegger T.,
RA Winters P., Wipat-A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
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CC -----
DR EMBL; AF133817; AAD29687.1; -;
DR EMBL; AF076971; AAD48089.1; -;
DR EMBL; AF054842; AAF09093.1; ALT_INIT.
DR EMBL; AF054843; AAF09094.1; -;
DR EMBL; BC010968; AAH10968.1; -;
DR MGD; MGI:1346085; Insl5.
DR InterPro; IPR004825; Ins/IGF/relax.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 135 INSULIN-LIKE PROTEIN INSL5 B CHAIN
FT FT
FT PROPEP 49 114 CONNECTING PEPTIDE (POTENTIAL).
FT CHAIN 115 135 INSULIN-LIKE PEPTIDE INSL5 A CHAIN
FT FT
FT DISULFID 29 122 INTERCHAIN (BY SIMILARITY).
FT DISULFID 41 135 INTERCHAIN (BY SIMILARITY).
FT DISULFID 121 126 BY SIMILARITY.
SQ SEQUENCE 135 AA; 15524 MW; 05FF9A0F613DBF92 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LFLLLVL 362
| | | | |
DB 8 LFLLLVL 14

RESULT 13
19KD_MYCAV STANDARD; PRT; 161 AA.
AC P46733;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-FEB-1996 (Rel. 33, Last annotation update)
DE 19 kDa lipoprotein antigen precursor.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 2;
RX MEDLINE=933202760; PubMed=8454357;
RA Booth R.J., Williams D.L., Moudgil K.D., Noonan L.C.,
RA Grandison P.M., McKee J.J., Prestidge R.L., Watson J.D.;
RT "Homologs of Mycobacterium leprae 18-kilodalton and Mycobacterium
tuberculosis 19-kilodalton antigens in other mycobacteria";
RL Infect. Immun. 61:1509-1515(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Probable).
CC
CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM 19 kDa ANTIGEN.
CC
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CC -----
DR EMBL; L12235; AAA25346.1; -;
DR InterPro; IPR000437; ProLipoprot.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
KW Antigen; Membrane; Lipoprotein; Signal.
FT SIGNAL 1 21 PROBABLE.
FT CHAIN 22 161 19 KDA LIPOPROTEIN ANTIGEN.
FT LIPID 22 22 N-ACYL DIGLYCERIDE (PROBABLE).

SQ SEQUENCE 161 AA; 15504 MW; 78A180B1A1C100E4 CRC64;
Query Match 1.1%; Score 7; DB 1; Length 161;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 218 SSSTSPS 224
| | | | |
DB 36 SSSTSPS 42

RESULT 14
Y319_MYCGE STANDARD; PRT; 178 AA.
ID Y319_MYCGE
AC P47561;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG319.
GN MG319.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96011386; PubMed=7592348;
RA Reddy S.P., Rasmussen W.G., Baseman J.B.;
RT "Molecular cloning and characterization of an adherence-related
RT operon of Mycoplasma genitalium";
RL J. Bacteriol. 177:5943-5951(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium";
RL Science 270:397-403(1995).
RN [3]
RP SEQUENCE OF 34-141 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing";
RL J. Bacteriol. 175:7918-7930(1993).
CC
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CC -----
DR EMBL; L43097; AAA99944.1; -;
DR EMBL; U39712; AAC71541.1; -;
DR EMBL; U01769; AAD10587.1; -;
DR TIGR; MG319; -;
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 124 144 POTENTIAL.
SQ SEQUENCE 178 AA; 20556 MW; 1BC5FDA9DA4AE14 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 27 secs

Qy 357 FLLLVLV 363
| | | | |
Db 12 FLLLVLV 18

RESULT 15

DSBE_YERPE STANDARD; PRT; 188 AA.
AC Q8ZD52;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thiol:disulfide interchange protein dsbE (Cytochrome c biogenesis
protein ccmg).
GN DSBE OR CCMG OR YPO2740.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
CC -!- FUNCTION: Involved in disulfide bond formation. Catalyzes a late,
reductive step in the assembly of periplasmic c-type cytochromes,
probably the reduction of disulfide bonds of the apocytochrome c
to allow covalent linkage with the heme. Possible subunit of a
heme lyase (By similarity).
CC -!- SUBCELLULAR LOCATION: Mostly periplasmic; anchored in the inner
membrane (By similarity).
CC -!- SIMILARITY: BELONGS TO THE THIOREDUXIN FAMILY. DSBE SUBFAMILY.

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or send an email to license@isb-sib.ch).

DR EMBL; AJ414153; CAC92979.1; -
DR InterPro; IPR004799; DsbE.
DR InterPro; IPR000063; Thiored.
DR ProDom; PD003679; DsbE; 1.
DR TIGRFAMs; TIGR00385; dsbE; 1.
DR PROSITE; PS00194; THIOREDUXIN; 1.
KW Cytochrome c-type biogenesis; Redox-active center; Transmembrane;
KW Inner membrane; Complete proteome.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 POTENTIAL.
FT DOMAIN 31 188 PERIPLASMIC (POTENTIAL).
FT DISULFID 85 88 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 188 AA; 21072 MW; AEA1967477034A56 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 188;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 355 VLFLLVV 361
| | | | |
Db 16 VLFLLVV 22

Search completed: July 11, 2003, 15:54:16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:49:42 ; Search time 22 seconds
(without alignments)
2862.184 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTSPSSSTALASCSRIARR.....SOEASQTLLDSVYSHLPDLL 655

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	7.5	651	JC7705	death receptor-6 -
2	9	1.4	387	G82983	probable MFS trans
3	8	1.2	127	S65194	probable membrane
4	8	1.2	138	B27863	Ac hypothetical pr
5	8	1.2	180	T32764	hypothetical prote
6	8	1.2	222	T43500	hypothetical prote
7	8	1.2	271	G83554	hypothetical prote
8	8	1.2	283	D71130	probable oligopept
9	8	1.2	305	C82524	pyrroline-5-carbox
10	8	1.2	312	A82485	Iron(III) ABC tran
11	8	1.2	316	AD2470	hypothetical prote
12	8	1.2	407	S62492	hypothetical PMWP
13	8	1.2	425	C70450	conserved hypothet
14	8	1.2	485	T24201	hypothetical prote
15	8	1.2	507	S64507	probable membrane
16	8	1.2	647	T42579	capsid protein 35
17	8	1.2	683	T12123	NADH2 dehydrogenas
18	8	1.2	807	T02916	hypothetical prote
19	8	1.2	880	T48477	hypothetical prote
20	8	1.2	987	A54092	protein-tyrosine k
21	8	1.2	1251	T21389	hypothetical prote
22	7	1.1	72	A11026	hypothetical prote
23	7	1.1	86	B75465	probable cation tr
24	7	1.1	103	D72549	hypothetical prote
25	7	1.1	113	T33779	hypothetical prote
26	7	1.1	113	C88947	protein C397.3 [1
27	7	1.1	114	G82793	hypothetical prote
28	7	1.1	119	D84845	hypothetical prote
29	7	1.1	119	H87152	hypothetical prote

30	7	1.1	128	2	JQ1203	hypothetical 14k p
31	7	1.1	129	2	S65989	yybH protein - Bac
32	7	1.1	135	2	G72601	hypothetical prote
33	7	1.1	135	2	C72539	hypothetical prote
34	7	1.1	141	2	T19125	probable transposa
35	7	1.1	143	2	G97752	tolR protein limpo
36	7	1.1	150	2	C87517	dnaj-related prote
37	7	1.1	151	2	T16284	hypothetical prote
38	7	1.1	158	2	E86396	t3p11.14 protein -
39	7	1.1	160	2	D98138	probable transcrip
40	7	1.1	172	2	AF3149	transcription regu
41	7	1.1	174	2	F84338	hypothetical prote
42	7	1.1	177	2	AE1410	hypothetical prote
43	7	1.1	178	2	C64235	hypothetical prote
44	7	1.1	186	2	AF2205	hypothetical prote
45	7	1.1	188	2	AD0334	thiol,disulfide in

ALIGNMENTS

RESULT 1

JC7705

death receptor-6 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: JC7705

R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A:Title: Conservation of Death receptor-6 in avian and piscine vertebrates.

A:Reference number: JC7705; MUID:21308433; PMID:11414698

A:Accession: JC7705

A:Molecule type: mRNA

A:Residues: 1-651 <BRI>

A:Cross-references: GB:AF349908

C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily, and is involved in cell death and/or survival signaling cascade.

C:Genetics:

A:Gene: dr-6

C:Keywords: ovary

F:1-21/Domain: signal sequence #status predicted <SIG>

F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F:332-350/Domain: transmembrane #status predicted <TM>

F:410-475/Domain: death domain #status predicted <DED>

F:551-651/Region: conserved cytoplasmic #status predicted

Query Match

Best Local Similarity 7.5%; Score 49; DB 2; Length 651;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 ADHERAYAAHQHTIRGPEASLAQLISALRQHRNDVVVKIRGLMEDT 502

Db 435 ADHERAYAAHQHTIRGPEASLAQLISALRQHRNDVVVKIRGLMEDT 483

RESULT 2

G82983

probable MFS transporter PA5311 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G82983

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G82983

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-387 <STO>

A:Cross-references: GB:AE004943; GB:AE004091; NID:G9951615; PIDN:AA080696.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA5311

Query Match 1.4%; Score 9; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 IAGSLLLLG 34

|||||

Db 167 IAGSLLLLG 175

RESULT 3

S65194

probable membrane protein YPL182c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein P2235

C:Species: Saccharomyces cerevisiae

C:Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 19-Apr-2002

C:Accession: S65194

R:Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansorge, W.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S65183

A:Accession: S65194

A:Molecule type: DNA

A:Residues: 1-127 <BEN>

A:Cross-references: EMBL:Z73538; NID:g1370380; PID:e246911; PID:g1370381; GSPDB:GN00016;

A:Experimental source: strain S288C (AB972)

C:Genetics:

A:Gene: MIPS:YPL182c

A:Cross-references: SGD:S0006103

A:Map position: 16L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YPL182c

C:Keywords: transmembrane protein

F:43-59/Domain: transmembrane #status predicted <TM1>

F:90-106/Domain: transmembrane #status predicted <TM2>

Query Match

1.2%; Score 8; DB 2; Length 127;

Best Local Similarity 100.0%; Pred. No. 7.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 SSSTSPSP 225

|||||

Db 22 SSSTSPSP 29

RESULT 4

B27863

Ac hypothetical protein ORFa - maize (fragment)

C:Species: Zea mays (maize)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Sep-1993

C:Accession: B27863

R:Kunze, R.; Stochaj, U.; Laufs, J.; Starlinger, P.

EMBO J. 6, 1555-1563, 1987

A:Title: Transcription of transposable element Activator (Ac) of Zea mays L.

A:Reference number: A91069

A:Accession: B27863

A:Molecule type: mRNA

A:Residues: 1-138 <KUN>

C:Superfamily: hypothetical transposase Ac9

Query Match

1.2%; Score 8; DB 2; Length 138;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10

|||||

Db 69 TSPSSSTA 76

RESULT 5

T32764

hypothetical protein F33D11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32764

R:Sammons, L.; Wohldmann, P.; Mullen, G.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid F33D11.

A:Reference number: Z21222

A:Accession: T32764

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-180 <SAM>

A:Cross-references: EMBL:AF039720; PIDN:AB96698.1; GSPDB:GN00019; CESP:F33D11.4

A:Experimental source: strain Bristol N2; clone F33D11

C:Genetics:

A:Gene: CESP:F33D11.4

A:Map position: 1

A:Introns: 68/1; 99/1; 153/3

Query Match

1.2%; Score 8; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 9.6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 SFSSSTSP 223

|||||

Db 63 SFSSSTSP 70

RESULT 6

T43500

hypothetical protein DKF2p586G1721.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T43500

R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, December 1999

A:Reference number: Z22515

A:Accession: T43500

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-222 <AAA>

A:Cross-references: EMBL:AL133642

A:Experimental source: adult uterus; clone DKF2p586G1721

C:Genetics:

A:Note: DKF2p586G1721.1

Query Match

1.2%; Score 8; DB 2; Length 222;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 STSPSPGT 227

|||||

Db 140 STSPSPGT 147

RESULT 7

G83554

hypothetical protein PA0735 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83554

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G83554

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-271 <STO>

A:Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AG04124.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0735

RESULT 12

S62492
hypothetical PMP domain-containing protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
A:Accession: S62492; T38277
R:Niblett, D.; Harris, D.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62492
A:Accession: S62492
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <NIB>
A:Cross-references: EMBL:Z64354; NID:g1039338; PIDN:CAA91236.1; PID:g1039339
R:Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21783
A:Accession: T38277
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-407 <NIB>
A:Cross-references: EMBL:Z64354; PIDN:CAA91236.1; GSPDB:GN00066; SPDB:SPAC23D3.01
A:Experimental source: strain 972h-; cosmid c23D3
C:Genetics:
A:Gene: SPAC23D3.01
A:Map position: 1R

Query Match 1.2%; Score 8; DB 2; Length 407;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 SPSPISP 526

Db 236 SPSPISP 243
|||||||

RESULT 13

C70450
conserved hypothetical protein aq_1743 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: C70450
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70450
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-425 <AQF>
A:Cross-references: GB:AE000754; NID:g2984047; PIDN:AAC07601.1; PID:g2984060; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_1743

Query Match 1.2%; Score 8; DB 2; Length 425;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 LLVLVVIV 366

Db 9 LLVLVVIV 16
|||||||

RESULT 14

T24201
hypothetical protein R12G8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24201
R:Basham, V.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19853

A:Accession: T24201

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-485 <WIL>

A:Cross-references: EMBL:Z93782; PIDN:CAB07854.1; GSPDB:GN00023; CESP:R12G8.2

A:Experimental source: clone R12G8

C:Genetics:

A:Gene: CESP:R12G8.2

A:Map position: 5

A:Introns: 74/1; 162/3; 210/1; 288/1; 339/3; 426/3

Query Match 1.2%; Score 8; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 STSSGSSA 569

Db 397 STSSGSSA 404
|||||||

RESULT 15

S64507
probable membrane protein YGR189c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G7553
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C:Accession: S64507
R:Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64499
A:Accession: S64507
A:Molecule type: DNA
A:Residues: 1-507 <ARR>
A:Cross-references: EMBL:Z72974; NID:g1323335; PID:e243566; PID:g1323336; GSPDB:GN000
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:CRH1; MIPS:YGR189c
A:Cross-references: SGD:S0003421
A:Map position: 7R
C:Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TM>

Query Match 1.2%; Score 8; DB 2; Length 507;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10

Db 356 TSPSSSTA 363
|||||||

Search completed: July 11, 2003, 15:53:46

Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:47:53 ; Search time 88 Seconds
(without alignments)
1533.646 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTPSPSSSTALASCRIARR.....SQBASQTLLDSVYSHLPDLL 655

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	49	7.5	83	Q8UWJ0	Q8UWJ0 gallus gall
2	49	7.5	651	Q98SM6	Q98SM6 gallus gall
3	9	1.4	387	Q9HTP3	Q9HTP3 pseudomonas
4	9	1.4	3396	Q3VM55	Q9VM55 drosophila
5	8	1.2	120	Q8SAZ1	Q8SAZ1 oryza sativ
6	8	1.2	127	Q8922	Q8922 saccharomyc
7	8	1.2	132	Q943G4	Q943G4 oryza sativ
8	8	1.2	180	Q9TZ27	Q9TZ27 caenorhabdi
9	8	1.2	219	Q9YXH9	Q9YXH9 human immun
10	8	1.2	222	Q4UF25	Q4UF25 homo sapien
11	8	1.2	240	Q98K49	Q98K49 rhizobium 1
12	8	1.2	271	Q915J4	Q915J4 pseudomonas
13	8	1.2	275	Q69051	Q69051 pseudomonas
14	8	1.2	283	Q58539	Q58539 pyrococcus
15	8	1.2	305	Q9PA08	Q9PA08 xylella fas
16	8	1.2	312	Q9KMU1	Q9KMU1 vibrio chol

17	1.2	314	10	O22440	O22440 oryza sativ
18	1.2	316	16	Q8YLI2	Q8YLI2 anabaena sp
19	1.2	345	10	Q949D2	Q949D2 oryza sativ
20	1.2	352	15	Q9WDC4	Q9WDC4 human immun
21	1.2	362	4	O95884	O95884 homo sapien
22	1.2	393	11	P70429	P70429 mus musculu
23	1.2	414	11	Q9ERU8	Q9ERU8 mus musculu
24	1.2	416	4	Q9UI08	Q9UI08 homo sapien
25	1.2	416	4	Q8TBV1	Q8TBV1 homo sapien
26	1.2	418	4	Q9UIC2	Q9UIC2 homo sapien
27	1.2	425	16	O67629	O67629 aquifex aeo
28	1.2	485	5	Q9XTV6	Q9XTV6 caenorhabdi
29	1.2	493	10	Q9LUS8	Q9LUS8 arabidopsis
30	1.2	572	11	Q9QZF6	Q9QZF6 rattus norv
31	1.2	577	10	Q9EXY7	Q9EXY7 artemisia a
32	1.2	586	10	Q94HX6	Q94HX6 oryza sativ
33	1.2	617	13	Q9IAA9	Q9IAA9 brachydanio
34	1.2	617	13	Q9PU64	Q9PU64 brachydanio
35	1.2	647	12	O39278	O39278 equine herp
36	1.2	683	8	O46936	O46936 saintpaulia
37	1.2	840	5	Q9N3Q5	Q9N3Q5 caenorhabdi
38	1.2	880	10	Q9LZ16	Q9LZ16 arabidopsis
39	1.2	935	4	Q96L35	Q96L35 homo sapien
40	1.2	949	10	Q9FMC9	Q9FMC9 arabidopsis
41	1.2	1021	5	Q8T811	Q8T811 dictyosteli
42	1.1	43	2	Q9K546	Q9K546 mycobacteri
43	1.1	53	2	Q93A11	Q93A11 thiobacillu
44	1.1	57	9	O56786	O56786 staphylococ
45	1.1	58	5	Q9VB42	Q9VB42 drosophila

ALIGNMENTS

RESULT 1

Q8UWJ0 PRELIMINARY; PRT; 83 AA.
AC Q8UWJ0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Death receptor 6 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RA Shi Z., Onagbesan O.M., Williams J.;
RT "Apoptosis in chicken ovary."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432512; AAL35560.1; -
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; Death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 9506 MW; 28F8C880F655FADC CRC64;

Query Match 7.5%; Score 49; DB 13; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 ADHERAYALQHWIRGPEASLAQLISALRQRRNDVYKIRGLMEDTT 502

DB 21 ADHERAYALQHWIRGPEASLAQLISALRQRRNDVYKIRGLMEDTT 69

RESULT 2

Q98SM6

```
ID Q98SM6 PRELIMINARY; PRT; 651 AA.
AC Q98SM6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RT Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL EMBL: AF349508; AKK29666.2;
DR HSP; P19438; INCF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR003975; Shal_channel.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 4.
DR PRINTS: PR01497; SHALCHANNEL.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;
Query Match 7.5%; Score 49; DB 13; Length 651;
Best Local Similarity 100.0%; Pred No. 1.4e-43;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 ADHERAYAAQLQHWIRGPASLAQLSALRQHRNDVVEKIRGLMEDTT 502
Db [1]
QY 435 ADHERAYAAQLQHWIRGPASLAQLSALRQHRNDVVEKIRGLMEDTT 483

RESULT 3
Q9HTP3 PRELIMINARY; PRT; 387 AA.
AC Q9HTP3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable MFS transporter.
GN PA5311.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RT STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goitry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL: AE004943; AAG08696.1;
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00083; sugar_tr; 1.
DR PROSITE: PS00402; BPD_TRANSP_INN_MEMBER; UNKNOWN_1.
KW Complete proteome.
```

```
SQ SEQUENCE 387 AA; 40522 MW; F898F53844EAA00B CRC64;
Query Match 1.4%; Score 9; DB 16; Length 387;
Best Local Similarity 100.0%; Pred No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 IAGSLLLLG 34
Db [1]
QY 167 IAGSLLLLG 175

RESULT 4
Q9VM55 PRELIMINARY; PRT; 3396 AA.
AC Q9VM55;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CG9138 protein.
GN SP1070 OR CG9138.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RT STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
CC -1- SIMILARITY: CONTAINS 3 CUB DOMAINS.
DR EMBL: AE003615; AAF52472.1;
DR HSP; P00740; 1EDM.
DR FlyBase: FBgn0031879; SPL070.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000859; CUB_domain.
```

DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR001092; HLHbasic.
 DR InterPro; IPR003410; Hyalin.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR002172; LDL_recept_A.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00431; CUB; 3.
 DR Pfam; PF00008; EGF; 17.
 DR Pfam; PF00734; FS_F8_type_C; 2.
 DR Pfam; PF02494; HVR; 3.
 DR Pfam; PF00057; ldl_recept_a; 1.
 DR Pfam; PF00084; sushi; 7.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00032; CCP; 8.
 DR SMART; SM00042; CUB; 3.
 DR SMART; SM00179; EGF_CA; 8.
 DR SMART; SM00001; EGF_like; 9.
 DR SMART; SM00231; FA58C; 2.
 DR SMART; SM00282; Lang; 1.
 DR SMART; SM00192; LDLa; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 11.
 DR PROSITE; PS01180; CUB; 6.
 DR PROSITE; PS00022; EGF_1; 15.
 DR PROSITE; PS01186; EGF_2; 13.
 DR PROSITE; PS01187; EGF_CA; 7.
 DR PROSITE; PS01285; FA58C_1; 1.
 DR PROSITE; PS01209; LDLRA_1; 1.
 DR PROSITE; PS50068; LDLRA_2; 2.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SQ SEQUENCE 3396 AA; 369389 MW; E618E9ACEA13E0E5 CRC64;

Query Match 1.4%; Score 9; DB 5; Length 3396;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 CPAGTYVSE 78
 |||||

Db 1694 CPAGTYVSE 1702

RESULT 5

ID Q8SAZ1 PRELIMINARY; PRT; 120 AA.
 AC Q8SAZ1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative dimethyladenosine transferase.
 GN OSUNBA0029P16.20.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
 RA Sasaki C., Henry D., Oates R., Simmons J., Wilson R., Mix P., Du H.;
 RT "Rice Genomic Sequence."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC093568; AAL78110.1; -;
 SQ SEQUENCE 120 AA; 12304 MW; A31240266825CE58 CRC64;
 Query Match 1.2%; Score 8; DB 10; Length 120;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 388 IVEKAGLK 395
 |||||
 Db 52 IVEKAGLK 59

RESULT 6

ID Q08922 PRELIMINARY; PRT; 127 AA.
 AC Q08922;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ORF YPL182C.
 GN YPL182C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benes V., Rechmann S., Nentwich U., Voss H., Ansoorge W.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z73538; CAA97890.1; -;
 DR SGD; S0006103; YPL182C.
 SQ SEQUENCE 127 AA; 13208 MW; A8FB6A243A7F7336 CRC64;

Query Match 1.2%; Score 8; DB 3; Length 127;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 SSSTSPSP 225
 |||||
 Db 22 SSSTSPSP 29

RESULT 7

ID Q943G4 PRELIMINARY; PRT; 132 AA.
 AC Q943G4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE P0046E05.16 protein (P0435B05.2 protein).
 GN P0046E05.16 OR P0435B05.2.
 OS Oryza sativa (Rice), and
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530, 39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0046E05.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0435B05.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003237; BAB67909.1; -;
 DR EMBL; AP003249; BAB89525.1; -;
 SQ SEQUENCE 132 AA; 12926 MW; C78D583ACB723D31 CRC64;
 Query Match 1.2%; Score 8; DB 10; Length 132;

Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 IVEKAGLK 395
DB 81 IVEKAGLK 88
|||||

RESULT 8
Q9TZ27 PRELIMINARY; PRT; 180 AA.
ID Q9TZ27;
AC Q9TZ27;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 20.3 kDa protein.
GN F33D11.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.,"
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Sammons L., Wohldmann P., Mullen G.;
RT "The sequence of C. elegans cosmid F33D11.,"
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.,"
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF039720; AAB96698.1; -;
DR HSSP; P02836; LENH.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH repressr.
DR Pfam; PF00046; homeobox.1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox.1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Hypothetical protein; Nuclear protein.
SQ SEQUENCE 180 AA; 20296 MW; FC2117756F8D4376 CRC64;

Query Match 1.2%; Score 8; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 SFSSSTSP 223
DB 63 SFSSSTSP 70
|||||

RESULT 9
Q9YXH9 PRELIMINARY; PRT; 219 AA.
ID Q9YXH9;
AC Q9YXH9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE -Gp120 (Fragment).

GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TZB0041;
RX MEDLINE=98252392; PubMed=9591718;
RA Renjifo B., Chaplin B., Mwakagile D., Shah P., Vannberg F.,
RA Wamanga G., Hunter D., Fawzi W., Essex M.;
RT "Epidemic expansion of HIV type 1 subtype C and recombinant genotypes
in Tanzania.,"
RL AIDS Res. Hum. Retroviruses 14:635-638(1998).
DR EMBL; AF038091; AAC98585.1; -;
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 24128 MW; E8C2187A57842751 CRC64;

Query Match 1.2%; Score 8; DB 15; Length 219;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 MNSTESNS 258
DB 123 MNSTESNS 130
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RESULT 10
Q9UF25 PRELIMINARY; PRT; 222 AA.
ID Q9UF25;
AC Q9UF25;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Hypothetical 22.4 kDa protein (Fragment).
GN DKFZP586G1721.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133642; CAB63763.1; -;
DR InterPro; IPR002965; P_rich_extensn.
DR PRINTS; PR01217; PRICHEXTENS.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 222 AA; 22369 MW; D0AF3E9C1C95EF95 CRC64;

Query Match 1.2%; Score 8; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 STSPSPGT 227
DB 140 STSPSPGT 147
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RESULT 11
Q98K49 PRELIMINARY; PRT; 240 AA.
ID Q98K49;
AC Q98K49;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Probable oxidoreductase.
GN MLR1638.


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OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002997; BAB48965.1; -.
DR InterPro; IPR002198; adh_short.
DR Pfam; PF00106; adh_short; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 24974 MW; 32EAF70467197083 CRC64;

Query Match 1.2%; Score 8; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TGOVLTC D 68
DB 226 TGOVLTC D 233
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RESULT 12
Q915J4 PRELIMINARY; PRT; 271 AA.
AC Q915J4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE Hypothetical protein PA0735.
GN PA0735.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004508; RAG04124.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 271 AA; 30821 MW; FAA5549CD4BD714E CRC64;

Query Match 1.2%; Score 8; DB 16; Length 271;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 IAGSLLL L 33
DB 10 IAGSLLL L 17
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RESULT 13
O69051 PRELIMINARY; PRT; 275 AA.
ID O69051

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O69051;
AC 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ATP-binding protein ptxA.
GN PtxA.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WM88;
RX MEDLINE=99008986; PubMed=97911102;
RA Metcalf W.W., Wolfe R.S.;
RT "Molecular genetic analysis of phosphite and hypophosphite oxidation
RT by Pseudomonas stutzeri WM88.";
RL J. Bacteriol. 180:5547-5558(1998).
CC -!- FUNCTION: PROBABLY FORMS PART OF A BINDING-PROTEIN-DEPENDENT
CC PHOSPHITE TRANSPORTER. REQUIRED FOR OXIDATION OF PHOSPHITE TO
CC PHOSPHATE.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF061070; AAC71706.1; -.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
FT NP_BIND 44 51 ATP (POTENTIAL).
SQ SEQUENCE 275 AA; 29649 MW; CC057CBE25A5B6BB CRC64;

Query Match 1.2%; Score 8; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 SALRQHR 487
DB 79 SALRQHR 86
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RESULT 14
O58539 PRELIMINARY; PRT; 283 AA.
AC O58539;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE 283AA long hypothetical oligopeptide transport permease protein APPC.
GN PH0809.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000003; BAA29902.1; -.
DR InterPro; IPR00515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 283 AA; 30664 MW; 922478741D15AF54 CRC64;

Query Match 1.2%; Score 8; DB 17; Length 283;

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Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 LLLVLVVI 365
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DB 24 LLLVLVVI 31

RESULT 15

Q9PA08 PRELIMINARY; PRT; 305 AA.
AC Q9PA08; 2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Pyroline-5-carboxylate reductase.
GN XF2712.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranos E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL: AE004077; AAF85509.1; -
DR InterPro: IPR000304; P5CR.
DR Pfam: PF01089; P5CR; 1.
DR TIGRFAMs: TIGR00112; proc; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 31918 MW; BD0803B6FC09AB5 CRC64;

Query Match 1.2%; Score 8; DB 16; Length 305;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 RATATMIA 27
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DB 8 RATATMIA 15

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-041-574-2

Perfect score: 3456

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3456	100.0	655	20	AAW41693 Human PRO868 prote
2	3456	100.0	655	20	AAW81059 Novel human tumor
3	3456	100.0	655	21	AAW26981 Human tumor necro
4	3456	100.0	655	21	AAW01349 Tumour necrosis fa
5	3456	100.0	655	21	AAW01338 DR-6 death recepto
6	3456	100.0	655	21	AAW77460 Human TNF receptor
7	3456	100.0	655	22	AAW29232 Human PRO polypept
8	3456	100.0	655	23	AAW21958 Human death domain
9	3456	100.0	691	21	AAW92846 Human osteoprotegr
10	3454	99.9	655	21	AAW44249 Human PRO868 (UNQ4

11	3450	99.8	655	19	AAW75792 Human tumour necro
12	3444	99.7	655	22	AAW93023 Human protein sequ
13	3342	96.7	631	20	AAW05678 Human full-length
14	3342	96.7	631	23	AAW21959 Human death domain
15	2892	83.7	605	20	AAW05697 Human TNF receptor
16	2723	78.8	573	20	AAW05695 Mouse TNF receptor
17	2573	74.5	508	20	AAW05680 Tumour necrosis fa
18	2544	73.6	600	21	AAW92845 Murine osteoprotegr
19	2233	64.6	444	21	AAW77461 Human TNF receptor
20	2091	60.5	405	21	AAW67947 Human DETH protein
21	2079	60.2	393	20	AAW28450 A human tumour nec
22	1365	39.5	254	21	AAW92843 Human osteoprotegr
23	1359	39.3	253	20	AAW05696 Human TNF receptor
24	1357	39.3	290	21	AAW92844 Human osteoprotegr
25	1354	39.2	290	21	AAW92842 Human osteoprotegr
26	1245	36.0	229	20	AAW05679 Human soluble tumo
27	1216	35.2	222	22	AAW56603 Human brain expres
28	1216	35.2	222	22	AAW16812 Peptide #3246 enco
29	1216	35.2	222	22	AAW29294 Peptide #3331 enco
30	1216	35.2	222	22	AAW04528 Peptide #3210 enco
31	1216	35.2	222	23	ABG38570 Human peptide enco
32	992	28.7	210	21	AAW77459 Human TNF receptor
33	934	27.0	164	21	AAW00012 Peptide fragment o
34	841	24.3	147	21	AAW26985 Human TNF receptor
35	673	19.5	125	19	AAW75793 Tumour necrosis fa
36	439	12.7	85	22	ABW29318 Peptide #1969 enco
37	439	12.7	85	22	ABW30755 Peptide #3406 enco
38	439	12.7	85	22	ABW35932 Peptide #3438 enco
39	439	12.7	85	22	ABW19901 Protein #1300 enco
40	439	12.7	85	22	ABW21341 Protein #3340 enco
41	439	12.7	85	22	AAW55278 Human brain expres
42	439	12.7	85	22	AAW56735 Human brain expres
43	439	12.7	85	22	AAW67675 Human bone marrow
44	439	12.7	85	22	AAW69113 Human bone marrow
45	439	12.7	85	22	AAW15484 Peptide #1918 enco

ALIGNMENTS

RESULT 1

AAW41693
ID AAW41693 standard; Protein; 655 AA.

XX AC AAW41693;

XX DT 07-DEC-1999 (first entry)

XX DE Human PRO868 protein sequence.

XX DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.

XX OS Homo sapiens.

XX PN WO9946281-A2.

XX PD 16-SEP-1999.

XX PF 08-MAR-1999; 99WO-US05028.

XX PR 10-MAR-1998; 98US-0077450.

XX PR 11-MAR-1998; 98US-0077632.

XX PR 11-MAR-1998; 98US-0077641.

XX PR 11-MAR-1998; 98US-0077649.

XX PR 12-MAR-1998; 98US-0077791.

XX PR 13-MAR-1998; 98US-0078004.

XX PR 17-MAR-1998; 98US-0040220.

XX PR 20-MAR-1998; 98US-0078886.

XX PR 20-MAR-1998; 98US-0078910.

XX PR 20-MAR-1998; 98US-0078936.

XX PR 20-MAR-1998; 98US-0078939.

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PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079556.
PR 27-MAR-1998; 98US-0079563.
PR 27-MAR-1998; 98US-0079564.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 31-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
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PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
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PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
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PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
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PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
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PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 05-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
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PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
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PR 15-MAY-1998; 98US-0085373.
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PR 22-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.

PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX (GETH ) GENENTECH INC.
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
DR N-PSDB; AA233945.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders
XX
PS Claim 12; Fig 26; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 655 AA;
Query Match 100.0%; Score 3456; DB 20; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.8e-274;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLLGLFLSTTTTAQPEKASNLIGTYRHVDRA 60
DB 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLLGLFLSTTTTAQPEKASNLIGTYRHVDRA 60
QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQCPWPWIEK 120
DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQCPWPWIEK 120
QY 121 LPCAALTDRETCPCPGMFOFNATCAPHTVCPVGWGVKKGTEDETRCQKARGTSDVP 180
DB 121 LPCAALTDRETCPCPGMFOFNATCAPHTVCPVGWGVKKGTEDETRCQKARGTSDVP 180
QY 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTATFPRPEHMETHE 240
DB 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTATFPRPEHMETHE 240
QY 241 VPSSTYVPGKMNSTESNSSASVRPKVLLSISQGTVPDNTSSARGKEDVNKTLPNLQVVNH 300
DB 241 VPSSTYVPGKMNSTESNSSASVRPKVLLSISQGTVPDNTSSARGKEDVNKTLPNLQVVNH 300
QY 301 QOQPHRHILKLLPSMEATGGEKSSPTPIKGRKRGHPQRNLKHFDINEHLPWMIIVLFLL 360
DB 301 QOQPHRHILKLLPSMEATGGEKSSPTPIKGRKRGHPQRNLKHFDINEHLPWMIIVLFLL 360
QY 361 VLWVIIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSWTPTONREKWIYYCNGHGDI 420
DB 361 VLWVIIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSWTPTONREKWIYYCNGHGDI 420
QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNGYTADHERAYAAALQHWTIIRGPASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNGYTADHERAYAAALQHWTIIRGPASLAQLIS 480
QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
QY 541 SPQDNKNGFFVDESEPLLRKCDSTSSGSSSALSRNGSFITKEKDTVLQRVLRDPCDLQPIF 600
```


cardiovascular disease; neurological disease; protein coordinate data.

Homo sapiens.

WO2000056862-A1.

28-SEP-2000.

16-MAR-2000; 2000WO-US06831.

24-MAR-1999; 99US-0126019.

14-MAY-1999; 99US-0134220.

(HUMA-) HUMAN GENOME SCI INC.

NI J, Gentz RL, Yu G, Fan P;

WPI; 2000-594575/56.

N-PSDB; AAA99638.

Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy and cancer -

Claim 20; Fig 1; 220pp; English.

The present sequence is a novel human tumor necrosis factor receptor, designated TR9. The TR9 receptor is also known as Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for treating, preventing or diagnosing common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and other neurological diseases.

Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 21; Length 655;

Best Local Similarity 100.0%; Pred. No. 6.8e-274;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60

DB 1 MGTSPSSSTALASCSRIARRATATMIAGSLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60

QY 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTRHENGIEKCHDCSQCPWPMEIK 120

DB 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTRHENGIEKCHDCSQCPWPMEIK 120

QY 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPGVGVRKKGTTEDVRCKQCARGTFSVDP 180

DB 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPGVGVRKKGTTEDVRCKQCARGTFSVDP 180

QY 181 SSVMKCKAYTDCLSQNLVVKPQTKETDNVCGTLPFSFSSSTSPSGTATFPRPEHMETHE 240

DB 181 SSVMKCKAYTDCLSQNLVVKPQTKETDNVCGTLPFSFSSSTSPSGTATFPRPEHMETHE 240

QY 241 VPSSTVYPKGMSTENSSASVRPKVLSSIQGTVPDNTSSARGEDVKNKTLPNQVNVH 300

DB 241 VPSSTVYPKGMSTENSSASVRPKVLSSIQGTVPDNTSSARGEDVKNKTLPNQVNVH 300

QY 301 QGPHHRHLKLLPSMEATGGKSTPIKGPXRGHPQNLKHFDINEHLPWMLVFLLL 360

DB 301 QGPHHRHLKLLPSMEATGGKSTPIKGPXRGHPQNLKHFDINEHLPWMLVFLLL 360

QY 361 VLWVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILK 420

DB 361 VLWVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILK 420

QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNSGTYADHERAYAAQLQHTWIRGPEASLAQLIS 480

Db 421 LVAAQVGSQWKDIYQFLCNASREVAAFNSGTYADHERAYAAQLQHTWIRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPNAKLENSALLTVEP 540

Db 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPNAKLENSALLTVEP 540

QY 541 SPQDKNKGFFVDESEPLLRCDSTSSGSSALSRLNGSFTITKEKDTVLQRVRLDPCDLQPIF 600

Db 541 SPQDKNKGFFVDESEPLLRCDSTSSGSSALSRLNGSFTITKEKDTVLQRVRLDPCDLQPIF 600

QY 601 DDLHLFNLPEELRVIEEIPQAEKLDRLFEIIGVKSQASQTLDSVYSHLPDLL 655

Db 601 DDLHLFNLPEELRVIEEIPQAEKLDRLFEIIGVKSQASQTLDSVYSHLPDLL 655

RESULT 4

AAB01349

ID AAB01349 standard; Protein; 655 AA.

XX

AC AAB01349;

XX

DT 20-OCT-2000 (first entry)

XX

DE Tumour necrosis factor receptor homologue TRH1 (Clone 2733717).

XX

KW Tumour necrosis factor receptor homologue; TRH1; TNF; arthritis;

KW transplant rejection; activation; proliferation; differentiation;

KW apoptosis; immunosuppression; antiinflammatory; immunostimulation;

KW probe; primer; human.

XX

OS Homo sapiens.

XX

PN WO200034294-A2.

XX

PD 15-JUN-2000.

XX

PF 10-DEC-1999; 99WO-US29400.

XX

PR 11-DEC-1998; 98US-0111826.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Bowen MA, Siemers N;

XX

DR WPI; 2000-423364/36.

XX

N-PSDB; AAA47395.

XX

PT Novel tumor necrosis factor receptor homologue-1 useful as a target for immunosuppressive, antiinflammatory and/or immunostimulatory drug development

XX

PS Claim 10; Fig 2a-2d; 42pp; English.

XX

CC The tumour necrosis factor receptor homologue TRH1 can be used for treating a mammal e.g. a human, at risk for a disorder characterized by an aberrant or unwanted level or biological activity of TRH1, e.g. rheumatoid arthritis and transplant rejection. TRH1 may also be useful to leach out or block a ligand which is found to bind to the TRH1. TRH1 may be used in various drug screening techniques and to identify fragments and analogs of a protein or peptide (agonist or antagonist) which bind to TRH1. The TRH1 protein plays a role in cellular function, cell activation, proliferation, differentiation, and apoptosis. The interaction between the novel TNFR protein of the present invention and intracellular signaling molecules and/or its potential co-receptor may serve as a novel target for immunosuppressive, antiinflammatory and/or immunostimulatory drug development. Gene constructs can also be used as part of a gene therapy protocol to deliver nucleic acids encoding the TRH1, or an agonist or antagonist form of a TRH1 protein or peptide. Antibody directed against TRH1 can be used to reject TRH1 in tissues and cells. They can also be used to make targeted antibody that destroy TRH1 expressing cells. Fragments of the TRH1 gene can be used as diagnostic probes or as PCR primers. Fragments of the full

CC length gene may be used as hybridization probes for a cDNA library to
CC isolate the full length gene and to isolate other genes which have a
CC high sequence similarity. The probes may be used to identify a cDNA
CC clone corresponding to a full length transcript and a genomic clone
CC or clones that contain the complete gene including regulatory and
CC promoter regions, exons, and introns.
XX
SQ Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 21; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.8e-274;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
QY 61 TGOVLTCDCPCAGTIVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMEK 120
DB 61 TGOVLTCDCPCAGTIVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMEK 120
QY 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPVGWGRKKGTTEDVRCQKARGTFSDVP 180
DB 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPVGWGRKKGTTEDVRCQKARGTFSDVP 180
QY 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
DB 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
QY 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPLNQVNH 300
DB 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPLNQVNH 300
QY 301 QOGPHRHRLKLLPSMEATGGEKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360
DB 301 QOGPHRHRLKLLPSMEATGGEKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360
QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHGIDILK 420
DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHGIDILK 420
QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPSPNAKLENSALLTVEP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPSPNAKLENSALLTVEP 540
QY 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKDTVLRLQVRLDPCDLQPIF 600
DB 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKDTVLRLQVRLDPCDLQPIF 600
QY 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQILLDSVYSHLPDLL 655
DB 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQILLDSVYSHLPDLL 655

RESULT 5
ID AAB01338 standard; Protein; 655 AA.
XX AC AAB01338;
XX DT 25-SEP-2000 (first entry)
XX DE DR-6 death receptor.
XX KW ULI144; death receptor; apoptosis; programmed cell death; FAS;
KW TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
XX human.
XX OS Homo sapiens.

XX WO200034335-A2.
XX 15-JUN-2000.
XX 03-DEC-1999; 99WO-US26035.
XX 04-DEC-1998; 98US-0205018.
XX (SCHE) SCHERING CORP.
XX Leong C, Phillips JH;
XX WPI; 2000-423383/36.
XX Purified or recombinant polypeptide for modulating apoptosis comprises
XX a sequence which binds to an antibody specific for ULI144 or its
XX fragments
XX Disclosure; Page 68-70; 76pp; English.
XX A pure or recombinant polypeptide which binds to a polyclonal antibody
XX specific for the mature ULI144 is useful for screening molecules which
XX block induction of apoptosis or interfere with antiapoptotic activity.
XX The polypeptide is also useful for modulating apoptosis and useful in
XX treatment of conditions associated with abnormal physiology or
XX development, such as cancer or degenerative conditions and for
XX regulation of viral infection and replication. At least five
XX different death receptors are known, which include the CD95
XX (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
XX protein (TRAMP), death receptor-6 (DR-6), and TNF-related
XX apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
XX SQ Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 21; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.8e-274;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
QY 61 TGOVLTCDCPCAGTIVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMEK 120
DB 61 TGOVLTCDCPCAGTIVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMEK 120
QY 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPVGWGRKKGTTEDVRCQKARGTFSDVP 180
DB 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPVGWGRKKGTTEDVRCQKARGTFSDVP 180
QY 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
DB 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
QY 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPLNQVNH 300
DB 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPLNQVNH 300
QY 301 QOGPHRHRLKLLPSMEATGGEKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360
DB 301 QOGPHRHRLKLLPSMEATGGEKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360
QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHGIDILK 420
DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHGIDILK 420
QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPSPNAKLENSALLTVEP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPSPNAKLENSALLTVEP 540

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; cervix; liver; genetic disorder.
 OS
 XX Homo sapiens.

PN WO200168848-A2.
 XX 20-SEP-2001.
 XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 03-MAR-2000; 2000US-187202P.
 PR 06-MAR-2000; 2000US-186968P.
 PR 14-MAR-2000; 2000US-189320P.
 PR 14-MAR-2000; 2000US-189328P.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 21-MAR-2000; 2000US-190828P.
 PR 21-MAR-2000; 2000US-191007P.
 PR 21-MAR-2000; 2000US-191048P.
 PR 21-MAR-2000; 2000US-191314P.
 PR 28-MAR-2000; 2000US-192655P.
 PR 29-MAR-2000; 2000US-193032P.
 PR 29-MAR-2000; 2000US-193053P.
 PR 30-MAR-2000; 2000WO-US0843P.
 PR 04-APR-2000; 2000US-194449P.
 PR 04-APR-2000; 2000US-194647P.
 PR 11-APR-2000; 2000US-195975P.
 PR 11-APR-2000; 2000US-196000P.
 PR 11-APR-2000; 2000US-196187P.
 PR 11-APR-2000; 2000US-196690P.
 PR 11-APR-2000; 2000US-196820P.
 PR 18-APR-2000; 2000US-198121P.
 PR 18-APR-2000; 2000US-198585P.
 PR 25-APR-2000; 2000US-199397P.
 PR 25-APR-2000; 2000US-199550P.
 PR 25-APR-2000; 2000US-199654P.
 PR 03-MAY-2000; 2000US-201516P.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 05-JUN-2000; 2000US-209832P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 22-AUG-2000; 2000US-0644848.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.

PA (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PU, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-602746/68.

DR N-PSDB; AAS46133.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumours, such as prostate and breast tumours, in mammals and
 PT to screen for modulators of the compounds -

XX Claim 11; Fig 418; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats

CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders.

XX Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 22; Length 655;
 Best Local Similarity 100.0%; Pred. No. 6.8e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGTSPSSSTALASCRIARRATATATMIAGSLLLGLFLSTTTAQPQKASNLGTYRHVDRA	60
Db	1	MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPQKASNLGTYRHVDRA	60
Qy	61	TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCSPCPWPMLEK	120
Db	61	TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCSPCPWPMLEK	120
Qy	121	LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTETEDVRCCKCARGTFSVDP	180
Db	121	LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTETEDVRCCKCARGTFSVDP	180
Qy	181	SSVMKCKAYTCLSQLNVLVVKPGTKETDNVCGTLPSSSSSTSPSPGTAIFRPEHMETHE	240
Db	181	SSVMKCKAYTCLSQLNVLVVKPGTKETDNVCGTLPSSSSSTSPSPGTAIFRPEHMETHE	240
Qy	241	VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARGKEDVNTLPNLQVNNH	300
Db	241	VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARGKEDVNTLPNLQVNNH	300
Qy	301	QOGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRONLKHFDINLHPLPMIYVLFLL	360
Db	301	QOGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRONLKHFDINLHPLPMIYVLFLL	360
Qy	361	VLVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYCNHGHGIDILK	420
Db	361	VLVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYCNHGHGIDILK	420
Qy	421	LVAAGVGSQWKDIYQFLCNASEREVAAFSNYTDHERAYAAALQHWITRGPEASLAQLIS	480
Db	421	LVAAGVGSQWKDIYQFLCNASEREVAAFSNYTDHERAYAAALQHWITRGPEASLAQLIS	480
Qy	481	ALRQRRNDVVEKIRGLMEDTTQLETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP	540
Db	481	ALRQRRNDVVEKIRGLMEDTTQLETDKIALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP	540
Qy	541	SPQDKNGKGFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTVLROVRDPCDLQPIF	600
Db	541	SPQDKNGKGFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTVLROVRDPCDLQPIF	600
Qy	601	DDMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAASQTLDSVYSHLPDLL	655
Db	601	DDMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAASQTLDSVYSHLPDLL	655

RESULT 8

AAE21958

ID AAE21958 standard; Protein; 655 AA.

XX AC AAE21958;

XX XX 25-JUL-2002 (first entry)

XX DE Human death domain containing receptor (DR6) protein.

XX KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
 KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;

diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis; transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis; autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic; H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide; acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus; HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective; adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic; dermatological; hepatotropic; antibacterial.

Homo sapiens.

Key Location/Qualifiers
 Peptide I..41
 Protein /label= Signal_peptide
 41..655
 Domain /note= "Mature human DR6"
 39..76
 Domain /note= "TNFR cysteine rich domain"
 77..118
 Domain /note= "TNFR cysteine rich domain"
 119..162
 Domain /note= "TNFR cysteine rich domain"
 163..201
 Domain /note= "TNFR cysteine rich domain"
 339..351
 Domain /note= "Transmembrane domain"
 360..370
 Domain /note= "Transmembrane domain"

WO200185209-A2.

15-NOV-2001.

30-APR-2001; 2001WO-US11735.

10-MAY-2000; 2000US-203015P.

(ELIL) LILLY & CO ELI.

Heuer JG, Liu J, Na S, Song HY, Yang D;

WPI: 2002-351283/38.

N-PSDB; AAD35053.

Treating or preventing T cell or Th2 cell mediated condition e.g., asthma or multiple sclerosis in mammal, comprises administering composition comprising death domain containing receptor, DR6 agonist or antagonist -

Claim 11; Page 126-129; 133pp; English.

The invention relates to a method for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. The method comprising administering to the mammal a pharmaceutical composition comprising a death domain containing receptor (DR6) agonist or antagonist. The method is useful for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing lung disease, organ rejection after transplantation, thrombotic thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS) or a condition or symptom related to the above mentioned diseases in a mammal. An DR6 antagonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with immunodeficiency, aberrant apoptosis, bacterial, viral or microbial

infection, complications of infection, human immunodeficiency virus (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori associated ulceration, cytoprotection during cancer treatment, recuperation from chemotherapy, recuperation from irradiation therapy, or a condition or symptom related to the above mentioned diseases in a mammal. The present sequence is human DR6 protein.

Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 23; Length 655;
 Best Local Similarity 100.0%; Pred. No. 6.8e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQEQKASNLCTGYRHVDRA 60
 DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQEQKASNLCTGYRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQCPWPPIEK 120
 DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQCPWPPIEK 120
 QY 121 LPCAALTIRECTCPGCMFOSNATCAPHTVCPVGWGVKKGTTEDVRCQCARGTSDVP 180
 DB 121 LPCAALTIRECTCPGCMFOSNATCAPHTVCPVGWGVKKGTTEDVRCQCARGTSDVP 180
 QY 181 SSMCKKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPCTATFPRPEHMETHE 240
 DB 181 SSMCKKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPCTATFPRPEHMETHE 240
 QY 241 VPSSTYVPGKMNSTESNSSASVPRKVLSSIQEGTVPDNTSSARGKEDVNKTLNQLQVNH 300
 DB 241 VPSSTYVPGKMNSTESNSSASVPRKVLSSIQEGTVPDNTSSARGKEDVNKTLNQLQVNH 300
 QY 301 QOGPHRHHTLLKLLPSWEATGGEKSTPIKGPGRHPRQNLHKHFDINEHLPMWVLFLL 360
 DB 301 QOGPHRHHTLLKLLPSWEATGGEKSTPIKGPGRHPRQNLHKHFDINEHLPMWVLFLL 360
 QY 361 VLVWIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYCHNGHGDILK 420
 DB 361 VLVWIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYCHNGHGDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITRGPEASLAQLIS 480
 DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITRGPEASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSNGSFITKEKKDTVLVRQLRDPCLQPIF 600
 DB 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSNGSFITKEKKDTVLVRQLRDPCLQPIF 600
 QY 601 DDMLHFLNPEELRVEETIQAEDKLDRLFEIIGVKVSQEAQTLLDSVSHLPDLL 655
 DB 601 DDMLHFLNPEELRVEETIQAEDKLDRLFEIIGVKVSQEAQTLLDSVSHLPDLL 655

RESULT 9

AA92846

ID AAY92846 standard; Protein; 691 AA.

XX AAY92846;

AC AAY92846;

XX 29-AUG-2000 (first entry)

XX Human osteoprotegrin-like 4 (OPGx4) protein.

DE OPGx4; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;
 KW inhibitor; bone resorption; vascular calcification; apoptosis;
 KW osteopathic.

XX* Homo sapiens.

OS Key Location/Qualifiers

XX Peptide 1..36

FT /note= "36 amino acid extension relative to

FT DR6 TNF-related death receptor"

XX

XX WO200024771-A2.

XX

XX 04-MAY-2000.

XX

XX 22-OCT-1999; 99WO-US24913.

XX

XX 23-OCT-1998; 98US-0105481.

XX 01-OCT-1999; 99US-0156993.

XX 21-OCT-1999; 99US-0422680.

XX (CURA-) CURAGEN CORP.

XX

XX Shinkets RA, Yang M, Lichenstein H, McDonald WF;

XX

XX WPI: 2000-350692/30.

XX N-PSDB: AAA28728.

XX

XX Nucleic acids encoding osteoprotegerin-like (OPGx) polypeptides, useful

XX for treating disorders associated with bone metabolism, such as

XX osteoporosis and osteopetrosis

XX

XX Claim 24; Fig 2; 81pp; English.

XX

XX Osteoprotegerin-like polypeptides (OPGx) are expressed in bone, lymph

XX node, germinal B cells and kidney. There appear to be at least two splice

XX variants of this gene, a transmembrane form and an extracellular domain

XX form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their

XX N-terminal relative to the DR6 tumour necrosis factor (TNF)-related death

XX receptor. The OPGx polypeptides, agonists and antibodies are useful in

XX methods to inhibit osteoclast-mediated bone resorption or vascular

XX calcification and to modulate cell death (apoptosis). This is useful for

XX treating disorders associated with bone metabolism, such as osteoporosis,

XX osteopetrosis, or a condition characterized by loss of bone, breakdown of

XX tissue, or excessive readorption of bone tissue.

XX

XX Sequence 691 AA;

XX

Query Match 100.0%; Score 3456; DB 21; Length 691;

Best Local Similarity 100.0%; Pred. No. 7.4e-274;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSPTSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPEKASNLIGTYRHVDRA 60

Db 37 MGTSPTSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPEKASNLIGTYRHVDRA 96

Qy 61 TGQVLTCDKCPAGYVSEHCTNTSLRVCSGCPVGTFTTRHENGIEKCHDCSQPCPWPMEK 120

Db 97 TGQVLTCDKCPAGYVSEHCTNTSLRVCSGCPVGTFTTRHENGIEKCHDCSQPCPWPMEK 156

Qy 121 LPCAALTDRECTCPGPFQSNATCAPHTVCPVGVGVKKTETEDVRCQCARCTFSDVP 180

Db 157 LPCAALTDRECTCPGPFQSNATCAPHTVCPVGVGVKKTETEDVRCQCARCTFSDVP 216

Qy 181 SSVNKKAYTDCLSLQNLVWIKPGTKETDNVCGTLPFSFSSSTSPSPGTAIFRPRPHMETHE 240

Db 217 SSVNKKAYTDCLSLQNLVWIKPGTKETDNVCGTLPFSFSSSTSPSPGTAIFRPRPHMETHE 276

Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGVTPDNTSSARGKEDVNKTLPLNLYVNH 300

Db 277 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGVTPDNTSSARGKEDVNKTLPLNLYVNH 336

Qy 301 QCGPHRHILKLLPSMEATGGEKSSSTPKGPKRGHPRQNLKHFDINEHLPWMLVFLLL 360

Db 337 QCGPHRHILKLLPSMEATGGEKSSSTPKGPKRGHPRQNLKHFDINEHLPWMLVFLLL 396

Qy 361 VLWVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGIDILK 420

Db 397 VLWVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGIDILK 456

Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTAADHERAYAAALQHWITIRGPEASLAOLIS 480

Db 457 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTAADHERAYAAALQHWITIRGPEASLAOLIS 516

Qy 481 ALROHRRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPNKLNSALLTVEP 540

Db 517 ALROHRRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPNKLNSALLTVEP 576

Qy 541 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVTLVLRQVRLDPCDLQPIF 600

Db 577 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVTLVLRQVRLDPCDLQPIF 636

Qy 601 DDMHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQTLDSVYSHLPDLL 655

Db 637 DDMHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQTLDSVYSHLPDLL 691

RESULT 10

AAB44249

ID AAB44249 standard; Protein; 655 AA.

XX

XX AAB44249;

XX

XX 08-FEB-2001 (first entry)

XX

XX Human PRO868 (UNQ437) protein sequence SEQ ID NO:64.

XX

XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;

XX expressed sequence tag; detection; cancer.

XX

XX Homo sapiens.

XX

XX WO2000053756-A2.

XX

XX 14-SEP-2000.

XX

XX 18-FEB-2000; 2000WO-US04341.

XX

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 29-MAR-1999; 99US-0126773.

XX 21-APR-1999; 99US-0130232.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 23-JUN-1999; 99US-0141037.

XX 26-JUL-1999; 99US-0145698.

XX 29-OCT-1999; 99US-0162506.

XX 30-NOV-1999; 99WO-US28313.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28565.

XX 16-DEC-1999; 99WO-US30095.

XX 30-DEC-1999; 99WO-US31243.

XX 30-DEC-1999; 99WO-US31274.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00277.

XX 06-JAN-2000; 2000WO-US00376.

XX

XX (GETH) GENENTECH INC.

XX

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gillisen ME;

XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

XX Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;

XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;

XX

XX WPI: 2000-611443/58.

XX DR N-PSDB: AAC78474.

XX

XX Novel PRO polypeptides and polynucleotides used in detection methods,

XX

PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 PS Claim 12; Fig 26; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 655 AA;
 Query Match 99.9%; Score 3454; DB 21; Length 655;
 Best Local Similarity 99.8%; Pred. No. 1e-273;
 Matches 654; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGTSPSSSTALASCRIARRATATMTAGSLLLLGLSTTTTAQPEQKASNLIGTYRHVDRA 60
 DB 1 MGTSPSSSTALASCRIARRATATMTAGSLLLLGLSTTTTAQPEQKASNLIGTYRHVDRA 60
 QY 61 TGOVLTCDCPKAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQCPWPMEIK 120
 DB 61 TGOVLTCDCPKAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQCPWPMEIK 120
 QY 121 LPCAALTDRECTCPGCMFOSNATCAPHTVPCVGMGVRKKGKTETEDVRCQKARGTFSDVP 180
 DB 121 LPCAALTDRECTCPGCMFOSNATCAPHTVPCVGMGVRKKGKTETEDVRCQKARGTFSDVP 180
 QY 181 SSVMKCKAYTDCLSQNLVVKGTETDNCVGTGLTFSSSTSPSGTATFPRPEHMETHE 240
 DB 181 SSVMKCKAYTDCLSQNLVVKGTETDNCVGTGLTFSSSTSPSGTATFPRPEHMETHE 240
 QY 241 VPSSTVYPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVH 300
 DB 241 VPSSTVYPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVH 300
 QY 301 QCGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHFDINEHLPWMLVFLLL 360
 DB 301 QCGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHFDINEHLPWMLVFLLL 360
 QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSWPTTONREKWIYICNGHGDILK 420
 DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSWPTTONREKWIYICNGHGDILK 420
 QY 421 LVAAQVGSQWKDIYFCLNASREVAFNGYTAADHERAYAAALQHWITIRGPASLAQLIS 480
 DB 421 LVAAQVGSQWKDIYFCLNASREVAFNGYTAADHERAYAAALQHWITIRGPASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPNKLNSALITVPEP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPNKLNSALITVPEP 540
 QY 541 SPQDNKGFVDESEPLLRCDSTSGSSALSRLNGSFITKEKDDTVLRQLRDLQPIF 600
 DB 541 SPQDNKGFVDESEPLLRCDSTSGSSALSRLNGSFITKEKDDTVLRQLRDLQPIF 600
 QY 601 DDLHLFNLPEELRVETEEIPOAEDKLDRLFEIIGVKSQEASQTLDSVYSHLPDLL 655
 DB 601 DDLHLFNLPEELRVETEEIPOAEDKLDRLFEIIGVKSQEASQTLDSVYSHLPDLL 655
 RESULT 11
 ID AAW75792 standard; Protein; 655 AA.
 XX
 AC AAW75792;

XX 21-DEC-1998 (first entry)
 DT Human tumour necrosis factor related receptor TR7.
 XX
 DE
 XX
 KW Tumour necrosis factor related receptor; TR7; human; inflammation;
 KW arthritis; septicemia; autoimmune disease; psoriasis;
 KW inflammatory bowel disease; infection; graft-versus-host disease;
 KW transplant rejection; stroke; acute respiratory disease syndrome;
 KW ischaemia; restenosis; brain injury; AIDS; bone disease; cancer;
 KW atherosclerosis; Alzheimer's disease; diagnosis; therapy; vaccine.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 24 /note= "encoded by ACG"
 FT
 XX
 PN EP869179-A1.
 XX
 PD 07-OCT-1998.
 XX
 PF 01-APR-1998; 98EP-0302528.
 XX
 PR 28-OCT-1997; 97US-0959382.
 PR 02-APR-1997; 97US-0041796.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Deen KC, Hurle MR, Tan KB, Young P;
 DR WPI; 1998-508493/44.
 DR N-PSDB; AAV57441.
 XX
 PT New tumour necrosis factor receptor TR7 polypeptides and
 PT polynucleotides - useful as diagnostic reagents and for treating
 PT Alzheimer's disease, AIDS and cancer
 XX
 PS Claim 11; Page 19-21; 25pp; English.
 XX
 CC This is the amino acid sequence of a novel member of the human
 CC tumour necrosis factor (TNF) receptor superfamily, termed TR7.
 CC It was deduced from the coding regions of overlapping isolated
 CC cDNA clones (see AAV57441). Expression systems, host cells and a
 CC method of producing TR7 polypeptides are claimed. TR7 polypeptides
 CC are useful for diagnosing diseases or susceptibility to diseases by
 CC determining TR7 polypeptide or mRNA expression. TR7 polypeptide
 CC can be used to screen for agonists and antagonists which bind the
 CC receptor. These can be used in treatment to inhibit or enhance TR7
 CC activity. TR7 antibodies are generated using TR7 polypeptide
 CC fragments, and are used for treatment of diseases. TR7 polypeptides
 CC and polynucleotides can be administered directly as vaccines for
 CC prevention of diseases. Diseases diagnosed, treated or prevented
 CC by the above methods include: chronic and acute inflammation,
 CC arthritis, septicemia, autoimmune diseases (e.g. inflammatory bowel
 CC disease, psoriasis), transplant rejection, graft vs. host disease,
 CC infection, stroke, ischaemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
 CC lymphoproliferative disorders), atherosclerosis, and Alzheimer's
 CC disease.
 XX
 SQ Sequence 655 AA;
 Query Match 99.8%; Score 3450; DB 19; Length 655;
 Best Local Similarity 99.8%; Pred. No. 2.1e-273;
 Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGTSPSSSTALASCRIARRATATMTAGSLLLLGLSTTTTAQPEQKASNLIGTYRHVDRA 60
 DB 1 MGTSPSSSTALASCRIARRATATMTAGSLLLLGLSTTTTAQPEQKASNLIGTYRHVDRA 60
 QY 61 TGOVLTCDCPKAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQCPWPMEIK 120
 DB 61 TGOVLTCDCPKAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQCPWPMEIK 120

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Db 61 TGOVLTCDKCPAGTYVSEHCNTNTSLRVCSSCPVGTFRHENGIEKCHDCSQCPWPMEK 120
Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Qy 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFRPRHEMETH 240
Db 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFRPRHEMETH 240
Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Qy 301 QOGPHRRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Db 301 QOGPHRRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Qy 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Db 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Qy 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
Db 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
Qy 541 SPQDNKGGFFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLOPIF 600
Db 541 SPQDNKGGFFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLOPIF 600
Qy 601 DDLHLFNLPEELRVEIIPQAEKDLRLFEIIGVKSQEASOTLLDSVYSHLPDLL 655
Db 601 DDLHLFNLPEELRVEIIPQAEKDLRLFEIIGVKSQEASOTLLDSVYSHLPDLL 655

RESULT 12
AAB93023
ID AAB93023 standard; Protein; 655 AA.
XX
AC AAB93023;
XX
DF 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:11787.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
XX
PR 27-AUG-1999; 99JP-0300253.
XX
PR 11-JAN-2000; 2000JP-0118776.
XX
PR 02-MAY-2000; 2000JP-0183767.
XX
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
```

```
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 11787; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where one of
CC an oligonucleotide comprising at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 655 AA;
```

Query Match 99.7%; Score 3444; DB 22; Length 655;

Best Local Similarity 99.7%; Pred. No. 6.6e-273;

Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPOKASNLIGTYRHHVDR 60
Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPOKASNLIGTYRHHVDR 60
Qy 61 TGOVLTCDKCPAGTYVSEHCNTNTSLRVCSSCPVGTFRHENGIEKCHDCSQCPWPMEK 120
Db 61 TGOVLTCDKCPAGTYVSEHCNTNTSLRVCSSCPVGTFRHENGIEKCHDCSQCPWPMEK 120
Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Qy 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFRPRHEMETH 240
Db 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFRPRHEMETH 240
Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Qy 301 QOGPHRRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Db 301 QOGPHRRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Qy 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Db 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Qy 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
Db 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
Qy 541 SPQDNKGGFFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLOPIF 600
Db 541 SPQDNKGGFFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLOPIF 600
```


Db 541 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRRNGSFITKEKDTVLRLQVRLDPCDLPQIF 600
QY 601 DDMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLDSVYSHLPDLL 655
|||||
Db 601 DDMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLDSVYSHLPDLL 655

RESULT 13

AA05678
ID AAY05678 standard; protein; 631 AA.

AC AAY05678;

XX 19-JUL-1999 (first entry)

DT Human full-length tumour necrosis factor receptor ZTNFR-6.

DE ZTNFR-6; tumour necrosis factor receptor-6; human;

KW cell maturation; bone cell regulation.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..17 /note- "signal peptide"

FT Protein 18..631 /note- "mature protein"

FT Protein 18..188 /note- "a polypeptide comprising this region of the

FT Protein 18..325 /note- "a polypeptide comprising this region of the

FT Protein 37..188 /note- "a polypeptide comprising this region of the

FT Protein 66..145 /note- "a polypeptide comprising this region of the

FT Protein 37..65 /note- "extracellular, cysteine-rich repeat"

FT Region 66..107 /note- "extracellular, cysteine-rich repeat"

FT Region 108..145 /note- "extracellular, cysteine rich repeat"

FT Region 146..188 /note- "extracellular, cysteine-rich repeat"

FT Region 189..325 /note- "linker region"

FT Domain 326..346 /note- "transmembrane domain"

FT Domain 347..631 /note- "cytoplasmic domain"

FT Domain 390..471 /note- "death domain, specifically claimed in

FT Claim 32(a)"

PN WO9911790-A1.

XX 11-MAR-1999.

XX 03-SEP-1998; 98WO-US18364.

PR 04-SEP-1997; 97US-0923725.

PR 04-SEP-1997; 97US-0057608.

XX (ZYMO) ZYMOGENETICS INC.

XX Farrah TM, Gross JA, Matthews SM;

PI WPI; 1999-205190/17.

DR N-PSDB; AAX25259.

XX

PT New secreted or membrane bound tumor necrosis factor receptor
XX ZTNFR-6 - useful for detecting a genetic abnormality in a patient
PS Claim 26; Page 113-115; 145pp; English.

CC The present sequence represents a novel human full-length
CC membrane-bound tumour necrosis factor receptor, designated ZTNFR-6,
CC that is characterised by 4 cysteine-rich pseudo-repeat motifs.
CC ZTNFR-6 polypeptides can be obtained using recombinant techniques.
CC A polynucleotide (see AAX25259) encoding ZTNFR-6 has been isolated
CC from an EST database. A secreted, soluble form (see AAY05679) of
CC ZTNFR-6 has also been identified, which lacks the transmembrane
CC and cytoplasmic domains of the membrane-bound protein. ZTNFR-6
CC polypeptides, including the isolated extracellular region,
CC transmembrane domain and death domain, are claimed. ZTNFR-6
CC polypeptides are useful in methods that promote cellular maturation
CC and bone cell regulation. Antibodies raised against ZTNFR-6 are
CC useful for immunohistochemical tagging of cells expressing ZTNFR-6
CC for use in diagnosis, isolating ZTNFR-6, generating anti-idiotypic
CC antibodies, and as neutralising antibodies or antagonists that block
CC ZTNFR-6 in vivo and in vitro. The polypeptides can also be used to
CC identify agonists and antagonists of ZTNFR-6. Agonists are useful
CC for modifying the proliferation and development of target cells in
CC vitro and in vivo.

XX Sequence 631 AA;

Query Match 96.7%; Score 3342; DB 20; Length 631;

Best Local Similarity 100.0%; Pred. No. 1.4e-264;

Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 MIAGSLLLLLGLFSTTTTAQPEQKASNLIGYRHHVDRATGQVLTCDKCPAGTYVSEHCNTS 84

DB 1 MIAGSLLLLLGLFSTTTTAQPEQKASNLIGYRHHVDRATGQVLTCDKCPAGTYVSEHCNTS 60

QY 85 LRVCCSCPVGTFTRHENGIEKCHDCSQCPWPWIEKLPCAAALTDRECTCPPGFMQSNATC 144

DB 61 LRVCCSCPVGTFTRHENGIEKCHDCSQCPWPWIEKLPCAAALTDRECTCPPGFMQSNATC 120

QY 145 APTVCVPGVGVRKKGTEDEVRCKOCARGTFSDVPSSVMKCKAYTDCLSQNLVLVTKPGT 204

DB 121 APTVCVPGVGVRKKGTEDEVRCKOCARGTFSDVPSSVMKCKAYTDCLSQNLVLVTKPGT 180

QY 205 KETDNYCGTLPSSFSSSTSPSGTAIFRPEHMETHEVPSTYVVKGMNSTESSASVRP 264

DB 181 KETDNYCGTLPSSFSSSTSPSGTAIFRPEHMETHEVPSTYVVKGMNSTESSASVRP 240

QY 265 KVLSSIQEGTVPDNTSSARGKEDVNTLPNLQVNVHQGPVHRRHILKLLPSMEATGCKS 324

DB 241 KVLSSIQEGTVPDNTSSARGKEDVNTLPNLQVNVHQGPVHRRHILKLLPSMEATGCKS 300

QY 325 STPIKGPGRGHPRQNLKHFIDNEHLPWMLVFLVLLVVLVVCSTRKSSRTLKKGPROD 384

DB 301 STPIKGPGRGHPRQNLKHFIDNEHLPWMLVFLVLLVVLVVCSTRKSSRTLKKGPROD 360

QY 385 PSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASERE 444

DB 361 PSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASERE 420

QY 445 VAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTOL 504

DB 421 VAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTOL 480

QY 505 ETDKALPMSPLSPSPSPNAKLENSALLTVPESPQDKNGKGFVDESEPLLRCDSTS 564

DB 481 ETDKALPMSPLSPSPSPNAKLENSALLTVPESPQDKNGKGFVDESEPLLRCDSTS 540

QY 565 SGSSALSRNGSFITKEKDTVLRLQVRLDPCDLPQIFDDMLHFLNPEELRVIEEIPQAEK 624

DB 541 SGSSALSRNGSFITKEKDTVLRLQVRLDPCDLPQIFDDMLHFLNPEELRVIEEIPQAEK 600

QY 625 LDRLFEIIGVKQSEASQTLDSVYSHLPDLL 655

|||||

601 LDRLEIIGVKQSEASOTLLDSVYSHLPDLL 631

Db-

RESULT 14

AAE21959
ID AAE21959 standard; Protein: 631 AA.

AA AAE21959;

XX 25-JUL-2002 (first entry)

XX Human death domain containing receptor (DR6) protein fragment.

XX Human; therapy: death domain containing receptor; DR6; receptor; anaemia;
KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
KW H. pylori-associated ulceration; anti-inflammatory; vasotropic; virucide;
KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;
KW dermatological; hepatotropic; antibacterial.

XX Homo sapiens.

XX WO200185209-A2.

XX 15-NOV-2001.

XX 30-APR-2001; 2001WO-US11735.

XX 10-MAY-2000; 2000US-203015P.

XX (ELIL) LILLY & CO ELI.

XX Heuer JG, Liu J, Na S, Song HY, Yang D;

XX WPI; 2002-351283/38.

XX Treating or preventing T cell or Th2 cell mediated condition e.g.,
PT asthma or multiple sclerosis in mammal, comprises administering
PT composition comprising death domain containing receptor, DR6 agonist or
PT antagonist.

XX Example 11; Page 129-131; 133pp; English.

XX The invention relates to a method for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. The
CC method comprising administering to the mammal a pharmaceutical
CC composition comprising a death domain containing receptor (DR6) agonist
CC or antagonist. The method is useful for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6
CC agonist is useful in the manufacture of a medicament for treating or
CC preventing at least one symptom associated with aberrant apoptosis,
CC graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma,
CC atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
CC insulin-dependent diabetes mellitus, cancer, multiple sclerosis,
CC Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic
CC lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
CC autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing
CC lung disease, organ rejection after transplantation, thrombotic
CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
CC for treating or preventing at least one symptom associated with
CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
CC infection, complications of infection, human immunodeficiency virus
CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori

CC associated ulceration, cytoprotection during cancer treatment,
CC recuperation from chemotherapy, recuperation from irradiation therapy,
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. The present sequence is human DR6 protein fragment.

XX Sequence 631 AA;

Query Match 96.7%; Score 3342; DB 23; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.4e-264;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 MIAGSLLLGLSTTTAQPQKASNLIGTRHVDVDRATQVLTCDKCPAGIYVSHCNTS 84
DB 1 MIAGSLLLGLSTTTAQPQKASNLIGTRHVDVDRATQVLTCDKCPAGIYVSHCNTS 60
QY 85 LRVCSGPCVGTFTTHENGIEKCHDCQPCWPMTLEKLPALCAALTDRECTCPGMEQSNATC 144
DB 61 LRVCSGPCVGTFTTHENGIEKCHDCQPCWPMTLEKLPALCAALTDRECTCPGMEQSNATC 120
QY 145 APHTVCPVGVGRKKGTTETEDVRCKQCARGTFSDVSSVMKCKAYTDCLSQNLVIRPGT 204
DB 121 APHTVCPVGVGRKKGTTETEDVRCKQCARGTFSDVSSVMKCKAYTDCLSQNLVIRPGT 180
QY 205 KETDNVCGTLPSPSSSTSPSPGTAIFRPRHEMETHETVPSTYVYPKGMNSTESNASVYP 264
DB 181 KETDNVCGTLPSPSSSTSPSPGTAIFRPRHEMETHETVPSTYVYPKGMNSTESNASVYP 240
QY 265 KVLSSIOEGTVPDNTSSARGKEDVNTLPNLQVNVHQGPHRHILKLLPSMEATGGEKS 324
DB 241 KVLSSIOEGTVPDNTSSARGKEDVNTLPNLQVNVHQGPHRHILKLLPSMEATGGEKS 300
QY 325 STPIKGPGRHPRQNLKHFDINEHLPWMIYVFLVLLVIVVCSIRKSSRTLKKGPRQD 384
DB 301 STPIKGPGRHPRQNLKHFDINEHLPWMIYVFLVLLVIVVCSIRKSSRTLKKGPRQD 360
QY 385 PSAIVERAGLKKSWPTQNRKWTYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASERE 444
DB 361 PSAIVERAGLKKSWPTQNRKWTYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASERE 420
QY 445 VAAFSNGYTADHERAYAAALQHTWIRGPEASLAQLISALRQHRNDVYVEKIRGLMEDTTOL 504
DB 421 VAAFSNGYTADHERAYAAALQHTWIRGPEASLAQLISALRQHRNDVYVEKIRGLMEDTTOL 480
QY 505 ETDKLALPMSPLSPSPPIPSNKLNSALLTVEPSPQDNKKGFFVDESEPLLRCDSTS 564
DB 481 ETDKLALPMSPLSPSPPIPSNKLNSALLTVEPSPQDNKKGFFVDESEPLLRCDSTS 540
QY 565 SGSSALSRNGSFITKEKKDVTLRQVRLDPCDLQPIFDDMLHFLNPEELRVTEETPQABDK 624
DB 541 SGSSALSRNGSFITKEKKDVTLRQVRLDPCDLQPIFDDMLHFLNPEELRVTEETPQABDK 600
QY 625 LDRLEIIGVKQSEASOTLLDSVYSHLPDLL 655
DB 601 LDRLEIIGVKQSEASOTLLDSVYSHLPDLL 631

RESULT 15

AAAY05697
ID AAAY05697 standard; Protein: 605 AA.

XX AAAY05697;

XX 19-JUL-1999 (first entry)

XX Human TNF receptor TRL II.

XX TRL II; TNF receptor-like; tumour necrosis factor receptor; human;
KW signal transduction; cell differentiation; prostate cancer;
KW inflammation; arthritis; diabetes; insulin resistance; diagnosis;
KW therapy.

XX Homo sapiens.

[illegible]

Search completed: July 11, 2003, 15:47:46
Job time : 49 secs

```

CC The present sequence represents human TRL II (TNF receptor-like), a
CC novel member of the tumour necrosis factor receptor superfamily.
CC The sequence is predicted from the sequence of a cDNA clone (see
CC AAX25322) isolated from an HeLa cell cDNA library. TRL II is a
CC a 66.2 kDa membrane-bound protein includes 4 cysteine-rich domains
CC and a C-terminal unique region containing a death domain. An
CC alternatively spliced secreted form, human TRL I (see AAX05696),
CC has also been identified. The invention provides full-length TRL
CC proteins, TRL fusion proteins, antigenic peptides and anti-TRL
CC antibodies, as well as TRL nucleic acids, recombinant expression
CC vectors, host cells and non-human transgenic animals. TRLs are
CC regulators or modulators of cellular signal transduction, cellular
CC proliferation or differentiation, cell survival and apoptosis,
CC immune system cells, and cells involved in insulin resistance or
CC the diabetic response. They can be used to isolate cognate
CC ligands, to modulate ligand/TRL interactions, to screen for
CC potential modulators, and to treat conditions associated with
CC abnormal TRL levels. Antibodies, TRL protein mutants etc. that
CC modulate activity of TRL are also used to treat/prevent conditions
CC associated with aberrant TRL protein or expression, e.g. cell
CC proliferation and differentiation disorders (particularly cancer,
CC especially of the prostate), inflammation (e.g. arthritis) and
CC metabolic disease (e.g. diabetes and insulin resistance).
CC
XX
SQ Sequence 605 AA;
Query Match 83.7%; Score 2892; DB 20; Length 605;
Best Local Similarity 100.0%; Pred. No. 9, 1e-228;
Matches 544; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 MGTSPSSSTALASCSRTARRATATMIAGSLLLGLFTTTTAQPPCKASNLIGTVRHVDRA 60
DB 1 MGTSPSSSTALASCSRTARRATATMIAGSLLLGLFTTTTAQPPCKASNLIGTVRHVDRA 60
QY 61 TGOVLTCDKCPAGTVYSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSCPWPMTKE 120

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:46:53 ; Search time 22 Seconds
(without alignments)
2862.184 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 3456

Sequence: 1 MGTPSSSTALASCRIARR.....SQEASQTLDSVSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2350	68.0	651	2 JC7705	death receptor-6 -
2	343.5	9.9	461	1 A35356	tumor necrosis fac
3	275.5	8.0	459	2 I48834	gene murine tumour
4	273.5	7.9	474	2 B38634	tumor necrosis fac
5	236.5	6.8	416	1 JN0006	nerve growth facto
6	235.5	6.8	255	2 I38426	lymphocyte activat
7	233	6.7	305	2 A46476	B cell-associated
8	228.5	6.6	435	2 I34182	tumor necrosis fac
9	218.5	6.3	326	1 GQVZML	T2 protein - myxom
10	211.5	6.1	325	2 B43692	nerve growth facto
11	211.5	6.1	425	1 A26431	nerve growth facto
12	210.5	6.1	427	1 GQHN	hypothetical prote
13	206.5	6.0	348	2 T28623	gene G4R protein -
14	206.5	6.0	349	2 D36858	CD30 antigen precu
15	205	5.9	595	2 A42086	G2R protein - vari
16	204.5	5.9	349	2 D72175	B-cell activation
17	200	5.8	277	2 A60771	tumor necrosis fac
18	193	5.6	461	2 J43302	hypothetical prote
19	191.5	5.5	2824	2 T22759	membrane glycoprot
20	187.5	5.4	493	2 JC5486	tumor necrosis fac
21	186.5	5.4	461	1 GQRT11	T-cell antigen 4-1
22	180.5	5.2	256	2 B32393	tumor necrosis fac
23	170	4.9	454	1 GQMT11	Ox40 homolog - hum
24	154	4.5	277	2 I37552	Ox40 antigen precu
25	148	4.3	271	2 S12783	tumor necrosis fac
26	145.5	4.2	455	1 GQHT11	laminin B2 chain
27	142.5	4.1	1193	2 A44018	hypothetical prote
28	138	4.0	1827	2 T34288	hypothetical prote
29	136.5	3.9	1205	2 T27053	hypothetical prote

30	136.5	3.9	1372	2 T25933	hypothetical prote
31	136	3.9	272	2 I48700	gene ox40 protein
32	135.5	3.9	5376	2 T42215	zonadhesin - mouse
33	132.5	3.8	1252	2 S36016	ocyst wall protei
34	129.5	3.7	3570	2 T45025	mucin MUC5B, trach
35	129	3.7	1459	2 T30196	kinesin motor prot
36	128.5	3.7	634	2 T00388	hypothetical prote
37	128.5	3.7	987	2 I48652	mouse developmenta
38	128.5	3.7	1032	2 T34433	hypothetical prote
39	128.5	3.7	2232	2 T34434	hypothetical prote
40	127.5	3.7	987	2 I48953	epn-related recept
41	126	3.6	1440	2 T27942	lin-15B protein -
42	125.5	3.6	1379	1 S01254	hepatocyte growth
43	123.5	3.6	557	2 A48434	variant-specific s
44	123.5	3.6	1367	1 S48478	glucan 1,4-alpha-g
45	123	3.6	2183	2 T42764	coagulation factor

ALIGNMENTS

RESULT 1

JC7705

Death receptor-6 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: JC7705

R:Bridgman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A:Reference number: JC7705; MUID:21308433; PMID:11414698

A:Accession: JC7705

A:Molecule type: mRNA

A:Residues: 1-651 <BRI>

A:Cross-references: GB:AF349908

C:Comment: This receptor, a member of the tumor necrosis factor receptor family, binds tressia, activates a cell death and/or survival signaling cascade.

C:Genetics:

A:Gene: dr-6

C:Keywords: ovary

F:1-21/Domain: signal sequence #status predicted <STG>

F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F:332-350/Domain: transmembrane #status predicted <TM>

F:410-475/Domain: death domain #status predicted <DED>

F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 68.0%; Score 2350; DB 2; Length 651;
Best Local Similarity 70.6%; Pred. No. 1.8e-148;
Matches 469; Conservative 47; Mismatches 102; Indels 46; Gaps 10;

QY	23	ATMTAGSLLGLGFLSTTTAQP----	EQKASNL-IGTYRHVDRTGQVLTCDKCPAGTVYS	77
DB	3	AAVLAALPLVLGLGTADAPKLTSEQNAVSLPAGKYLHLDRTATQOEICDKCPAGTVYS	62	
QY	78	EHCNTSLRVSSCPVGTFTREHNGIEKCHDCSPCPWPMEIKLPCCALTDRECTCPGPM	137	
DB	63	KHCYKSTLRESCPCPDGTFTHKENGIERCHPCRPCELPMEIKTCTALTDRCTCLSGT	122	
QY	138	FOSNATCAPHTVCPVGVGRKKGTETEDVRCKQARGTFSDVPSSVMCKKAYTDCLSQNL	197	
DB	123	FQINDTCVPYTVCPVGVGRKKGTETEDVRCKPCLRGTFSDVPSSVMCKKTYTDCFGKN	182	
QY	198	VVIRPGTKETDNCV---GTLP--SFSSSTSPGTAIFPRHEHMETHEVSPSTVYPKGMN	252	
DB	183	VVIRPGTKESDNCVSPASLPNTSLTSSDAQDG-----ETYEAPPTAYLPKGLN	232	
QY	253	STENSSASVRPKVLSIQEGTVDPNTSSARGKEDVKNLTPLNQLVNVNQQPHRHILKL	312	
DB	233	SSVFDLSSSPAPRVSNGTAEPTVDYNDTSANGTVGAPCSLSAGTAGOQSYRKHHTSQA	292	
QY	313	L---PSMEATGGEKSSPTIKGPKRGHPQNLKHFIDINEHLPWMIVLFLLLVIVVVC	369	
DB	293	MGKQPAQEMAGGKSSIPYRPPRGP--NVHQHFDINEHLPWMIVLFLLLVIVVVC	350	

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match	8.0%	Score	275.5	DB	2	Length	459		
Best Local Similarity	25.0%	Pred.	No. 9.7e-11						
Matches	82	Conservative	34	Mismatches	127	Indels	85	Gaps	10

QY	65	LTQDKCPAGYVSEHC	TNTSLRVCSSCPVGTFFRHENGIEKCHDCSQPCWPMTKEKLP	PCA	124
Db	38	MCCAKCPGGYVXHF	CNKNTSDTVCADCEASMYQVWNOFTCLJSCSSCSTDQVET	TRACT	97
QY	125	ALTDRECTCPGFMFQ	SNAT-----CAPHTVCPVGWGRVKKGTETEDVRCKQCCARGTFS	177	
Db	98	KQQRNVCACEAGRY	CALKTHSGSCRCMRLSCGPGFVASSRAPNGVNLCKACAPGTFS	157	
QY	178	DVPSVMKCKAYDCL	SQNLVWIKPGTKETDNNVCGTLPSFSSSTSPSPGTAIFRPR	EHME	237
Db	158	DTTSSTDVCRPHR	IC---SILAIPGNASTDAVCA-----PESPT	193	
QY	238	THEVPSSTYV---	PKGMNTESSNASSVPKKVLSSIOEGTVPDNTSSARGKEDV	NKTL	293
Db	194	LSAIPRLTVYSQPE	TRSQPLDQBPGPSPTSLTSL--GSTPIEQSTKG---GISLP	247	
QY	294	-----NLQVNN	-----HQGGPH-----HRRHLK	311	
Db	248	IGLIVGVTSLGLML	GLVNCFILVQRKKKPSCLQRDAKVPHVPDEKSDAVGLEQ	QHLLT	307
QY	312	LLPSMEATGKES	ST---PIRKPRKGRHP	337	
Db	308	TAPSSSSSSLESSA	SAGDRRAPPGGHPQ	335	

RESULT 4

B38634

tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

C:Accession: B38634; A40254; S54816

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.; Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor x

A:Reference number: A38634; MUID:91187885; PMID:1849278

A:Accession: B38634

A:Molecule type: mRNA

A:Residues: 1-474 <LEW>

A:Cross-references: GB:M60469; NID:q199827; PIDN:AAA39752.1; PID:q199828

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A:Reference number: A40254; MUID:91246168; PMID:1645445

A:Accession: A40254

A:Molecule type: mRNA

A:Residues: 1-474 <GOO>

A:Cross-references: GB:M60469; NID:q199827; PIDN:AAA39752.1; PID:q199828

R:Kissonerghis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.

submitted to the EMBL Data Library, May 1995

A:Description: Characterization of the promoter region of the murine p75-TNF receptor.

A:Reference number: S54816

A:Accession: S54816

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <KIS>

A; Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat
 C; Keywords: cytokine receptor; transmembrane protein
 F; 1-22/Domain: signal sequence #status predicted <SIG>
 F; 23-47/Product: tumor necrosis factor receptor type 2 #status predicted
 F; 40-77/Domain: NGF receptor repeat homology <NG1>
 F; 79-120/Domain: NGF receptor repeat homology <NG2>
 F; 166-203/Domain: NGF receptor repeat homology <NG4>

Query Match	7.9%; Score 273.5; DB 2; Length 474;
Best Local Similarity	25.0%; Pred. No. 1.4e-10;
Matches	82; Conservative 34; Mismatches 127; Indels 85; Gaps 10;
Qy	65 LTCDKCPAGTVSEHCINTSLRVCSSCPVGFTTRHENGIEKCHDCSQCPWPMTIEKLPCA 124
Db	53 MCCAKCPGGQVKKHFNKNTSDTVACDCAESMYTQVNWQFRCLSCSSCTTDQVEIRACT 112
Qy	125 ALTDRECTCPGPMQSNAT-----CAPHTVCPVGWGVKKGKTETEDVRCKQCARGFTFS 177
Db	113 KQNRVCACEAGRYCALKTHSGSCRCMRLSKCGPGFVSSRAPNGVNLKACACPGTFS 172
Qy	178 DVPSSVMKCAYTDCLSQNLVVIKPGYKETDNVCGTLPFSFSSSTSPSGTAIFRPRHME 237
Db	173 DTTSSSTDVCRPHRIC-----SILAIPGNASTDAVCA-----PESPT 208
Qy	238 THEYPSSTYV----PKGMNSTESNSSASVRPKVLSSIOEGTVDPNTSSARGKEDVKNKTL 293
Db	209 LSAIPRTLYVSQPEPTRSQPLDQEPGPSQTSILTSL--GSTPIEQSTKG----GISLP 262
Qy	294 -----NLQVNV-----HQQGPH-----HRRHLK 311
Db	263 IGLIVGVTSLGLMLGVNCLLYQRKKKPKSQLORDAKVPHVPDEKSQDVAQLEQOHLT 322
Qy	312 LLPSMENATGGEKST--PIKGPKRGHPR 337
Db	323 TAPSSSSSSLESSASAGDRRAPPGGHCP 350

RESULT. 5

JN0006
nerve growth factor receptor, low affinity precursor - chicken
N:Alternate names: NGF receptor
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0006; A60504
R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R
Neuron 2, 1123-1134, 1989
A:Title: Structure and developmental expression of the nerve growth factor receptor i
A:Reference number: JN0006; MUID:90166579; PMID:2560385
A:Accession: JN0006
A:Molecule type: mRNA
A:Residues: 1-416 <LAR>
A:Experimental source: embryonic chick brain
R:Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A:Title: Structure and developmental expression of the chicken NGF receptor.
A:Reference number: A60504; MUID:90152140; PMID:2154393
A:Accession: A60504
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Comment: This protein is thought to form a high-affinity receptor when it associate
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-416/Product: nerve growth factor receptor #status predicted <EXT>
F:21-239/Domain: extracellular #status predicted <EXT>
F:24-57/Domain: NGF receptor repeat homology <NG1>
F:59-100/Domain: NGF receptor repeat homology <NG2>
F:101-139/Domain: NGF receptor repeat homology <NG3>
F:141-181/Domain: NGF receptor repeat homology <NG4>

F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Domain: NGF receptor repeat homology <NG5>
F:252-273/Domain: NGF receptor repeat homology <NG6>
F:274-425/Domain: intracellular #status predicted <MEM>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 211.5; DB 1; Length 425;
Best Local Similarity 22.9%; Pred. No. 1.6e-06;
Matches 119; Conservative 59; Mismatches 196; Indels 145; Gaps 25;

QY 12 ASCSRATATATMIAGSLLLLGLSTTTAQPEQKASNLIGYRHVDRTGQVLTCDKCP 71
Db 6 AACSMADRL-----RLLLLILGVSSGGAKECTST--GLYTH----SGE--CCKACN 49
QY 72 AGTYVSEHTNTSLRVSSCPVG-TFTRHENGTEKCHDCSQCPWPMEKLPCCAAALTDRE 130
Db 50 LGEVGAQPC-GANQVCEPCLDNVTFSDVVSATECKPCTE-CLGLQSMASFCVEADDAV 107
QY 131 CTCPPGMFOSNAT--CAPHTVCPVGVGRKKGTETEDVRCKQCARGTFSVPSSVMKCKA 188
Db 108 CRCAYGYQDEETGHCACSVCEVSGSLVFSCODKQNTVCECEPCTGYSDEANHVDPCLP 167
QY 189 YTDCLSONLVKPGTKETDNVCGTLPSPSSSTSPGTAIPRPEHMETHEVPSSTYVP 248
Db 168 CTVC-EDTERQURECTPWDAECEEIPG-----RWIPRST-PP 203
QY 249 KGMNST-ESNSASVRPKVLSSTQETVDPDNTSSARGKEDVKNLPLNVQVNHQCPHHR 307
Db 204 EGSdstAPSTQPEVPE--QDLVSTVADMTVWG----- 238
QY 308 HILKLLPSMEATGGEKSPPIKPKRGKHPQNLKHFDINEHLPWMIVLFLVLLVIVV 367
Db 239 -----SSQPV--VTRG-TTDNL-----IP--VYCSILAAVVVGLV 268
QY 368 CSIR----KSSRTLKGPQDPSAIVEKAGLAKKSTPTONREKWIYCNCHGIDILKVA 423
Db 269 AVIAKRWNSCKQKOGANSRP-----VNQTPPEGEK-LHSDSGISVDSQSOLDH 317
QY 424 AQVGSQWK-----DIYQFLCNASEREVAAFSNGYTADH---ERAY----- 460
Db 318 QQTHQTASGQALKGDGNYLSPLTKREEVEKLLNGDTRHLAGELGYQPEHIDSFTE 377
QY 461 -----NALQHTWIRGPEASLAQLISALROHRRNDVVVEKI 494
Db 378 ACPVRALLASWGAQ-DSATFLDALLAALRRIRADIVESL 415

RESULT 12

GQHN

nerve growth factor receptor precursor, low affinity [validated] - human

N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 08-Dec-2000
C:Accession: A25218; A60204; S21689; I57638
R:Johnson, D.; Lanhahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218; MUID:87051725; PMID:3022937
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <GB>
A:Cross-references: GB:M14764; NID:g189204; PIDN:AA859544.1; PID:g189205
R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattman, G.; Thompson, S.; Grob, P.;
J. Neurochem, 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A:Reference number: A60204; MUID:87085574; PMID:3023363
A:Accession: A60204

A:Molecule type: protein
A:Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A:Experimental source: melanoma cell line A875
A:Note: this sequence has been corrected by a note added in proof to follow the nucle
R:Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor
A:Reference number: S21689; MUID:92198017; PMID:1372492
A:Accession: S21689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor recept
A:Reference number: I57638; MUID:89096903; PMID:2850481
A:Accession: I57638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Comment: This protein is thought to form a high-affinity receptor when it associate
C:Comment: This receptor undergoes both N- and O-linked glycosylation.
C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:120234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
F:29-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>
F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TRM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 210.5; DB 1; Length 427;
Best Local Similarity 22.8%; Pred. No. 1.8e-06;
Matches 116; Conservative 58; Mismatches 204; Indels 131; Gaps 22;

QY 21 ATATMIAGSLLLLGLSTTTAQPEQKASNLIGYRHVDRTGQVLTCDKCPAGTYVSEHC 80
Db 5 ATGRAMDGPRLLLLLGLVSLGGAKACP-TGLYTH----SGE--CCKACNLGEGVAQPC 57
QY 81 TMTSLRVSSC-PVGTFTRHENGIEKCHDCSQCPWPMEKLPCCAAALTDRECTCPGPMQ 139
Db 58 -GANQVCEPCLDSVTFSDVVSATEPCKPCTE-CVGLQSMASFCVEADDAVCRCAVGYQ 115
QY 140 SNAT--CAPHTVCPVGVGRKKGTETEDVRCKQCARGTFSVPSSVMKCKAYTDCLSQNL 197
Db 116 DETTCRCACRVCAGSLVFSCQDKQNTVCECPDGTVDSEANHVDPCLCTVC-EDTE 174
QY 198 VVIKPGTETDNC-----GTLPFSSTSPSPGTAIPRPEHMETHEVPSSTYV 247
Db 175 ROLRECTRWADAECIEPGRWITRTPPEGSDSTAPST-----QPEAPEQDLIASTVA 229
QY 248 PKGMNSTESNSASVRPK-----VLSSIQETVPDNTSSARGKEDVKNLPLN 295
Db 230 --GVTTVNGSQPVVTRGTTDLNLPVCSILAAVVVGLVAVIAKRWNSCKQKOGANS 287
QY 296 QVYNHQGPQPHRHILKLLPSMEATGGEK--SSTPIKPKRGKHPQNLKHFDINEHLP 353
Db 288 RPNVOTPPPE-----GKXLDSDGISVDS-----QSLH---DQPH---- 320
QY 354 IVFLFLLVIVVCSIRKSSRTLKGPQDPSAIVEKAGLAKKSTPTONREKWIYCN 413

Db 321 -----TQTASGQALKG-----DGGLYSSLPPAKREE----- 346
QY 414 HGIDILKIVAAQVSGWKDIYQFLCNASEREVAFAFNGYTTADHERAY-----AALQH 465
Db 347 -----VEKLLNGSAGDTWRHL-----AGELGQPEHIDSTHEACPVRAILLAS 389
QY 466 WTIRGPENASLAQLISALRQHRNDVVEKI 494
Db 390 WATQ-DSATLDALLAALRIQRAIDLVESL 417

RESULT 13

T28623
Hypothetical protein G2R - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: 220488; MUID:94088747; PMID:8264798
A:Accession: T28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 6.0%; Score 206.5; DB 2; Length 348;
Best Local Similarity 34.1%; Pred. No. 2.6e-06;
Matches 44; Conservative 12; Mismatches 66; Indels 7; Gaps 2;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVSSCPVGFTRHENGIEKCHDCSQPCPWPMEIKLPKA 124
Db 41 LCCLSCPPTGYASRLCDSKNTQTCTPCGSGGFTTSRNNHLPACLSGRCNSNQVETRSCN 100
QY 125 ALTDRECTCPGMP-----OSNATCAPHTVCPVGWGVKKGTTEDYRCKQCARGTFS 178
Db 101 TTHNRICBSPGYCLLKSGGCKACVSQTKCGIGYV-SGHTSVGDVICSPCGFGTYSH 159
QY 179 VPSSVMKCK 187
Db 160 TVSSADKCE 168

RESULT 14

D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
A:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
Submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:9456758; PIDN:CAA49137.1; PID:g457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Fro
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of variola virus xhoI F O H P
A:Reference number: S46888
A:Accession: S46888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOI>
A:Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA7540.1; PID:g516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.

FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protect
A:Reference number: S32385; MUID:93202281; PMID:8384129
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
A:Gene: G4R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 6.0%; Score 206.5; DB 2; Length 349;

Best Local Similarity 34.1%; Pred. No. 2.6e-06;
Matches 44; Conservative 12; Mismatches 66; Indels 7; Gaps 2;
QY 65 LTCDKCPAGTYVSEHCTNTSLRVSSCPVGFTRHENGIEKCHDCSQPCPWPMEIKLPKA 124
Db 42 LCCLSCPPTGYASRLCDSKNTQTCTPCGSGGFTTSRNNHLPACLSGRCNSNQVETRSCN 101
QY 125 ALTDRECTCPGMP-----OSNATCAPHTVCPVGWGVKKGTTEDYRCKQCARGTFS 178
Db 102 TTHNRICBSPGYCLLKSGGCKACVSQTKCGIGYV-SGHTSVGDVICSPCGFGTYSH 160
QY 179 VPSSVMKCK 187
Db 161 TVSSADKCE 169

RESULT 15

A42086
CD30 antigen precursor - human
N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
A:Accession: A42086
R:Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A:Title: Molecular cloning and expression of a new member of the nerve growth factor
A:Reference number: A42086; MUID:92154659; PMID:1310894
A:Accession: A42086
A:Molecule type: mRNA
A:Residues: 1-595 <DUR>
A:Cross-references: GB:M83554; NID:g180095; PIDN:AAA51947.1; PID:g180096
A:Experimental source: HUT-102 cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBIP:82090)
C:Genetics:
A:Gene: GDB:CD30; D1S166E
A:Cross-references: GDB:I31547; OMIM:153243
A:Map position: lp36-lp36
C:Superfamily: NGF receptor repeat homology
C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-383/Domain: extracellular #status predicted <EXT>
F:384-407/Domain: transmembrane #status predicted <TM>
F:408-595/Domain: intracellular #status predicted <CYT>
F:101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.9%; Score 205; DB 2; Length 595;

Best Local Similarity 20.2%; Pred. No. 6.6e-06;
Matches 131; Conservative 66; Mismatches 250; Indels 200; Gaps 24;
QY 30 LLLLG--FLSTTTAQPEOK--ASNLIGTYRH-VDRATQVLTCDKCPAGTYVSEHCTNTS 84
Db 5 LAALGLLFLGALRAFPQDRPFEDTCHGNPSHYDKAVRR--CCYRCPMGLFPTQCCPQP 62
QY 85 LRVSSCPVGFTRHENGIEKCHDCSQPCPWPMEIKLPKAALTDRECTCPGMP----- 138
Db 63 TDCRQKQCEPDYILDADRCTACVTCSDR---DLVEKTPCAWNSSRVCECFMFCSTSAV 119

```

QY 139 QSNATCAPHVCPVGVGVRKKGTETEDV-----RCKQCARGTF----- 176
Db 120 NSCARCFHSHVCPAGMIVKFPGTAKNTVCEPASPGVSPACASPENCKEPPSSGTPQAKP 179
QY 177 -----SDVPSSV----- 183
Db 180 TPVSPATSSASTMPVRGGTKLAQEAASKLFRAPDSPSSVGRPSDDGLSPTQPCPEGSD 239
QY 184 -----MKCKAYTDCILSONLVVVKPGTKETDNVCGTLPFSFSSSTSPSPGTA- 228
Db 240 CRQCEPDYLDAGRCTACVCSRDDLVKTPCANSSRTCECRPGMICATSNASCAR 299
QY 229 IFRPEHMETHEVPSTYVPKGMNSTESNASSVVRPKVLSSIOEGTVPDNTSSARGKEDV 288
Db 300 CVFYP-----ICAAETVTKPDQMAEKDTFEAPPL-----GTQPCDNCNTPENGAP 345
QY 289 NKTLPNLQVNVHOGPHRRHILKLLPSMEATGGEKSTPIKPKRGHPRONLHKHEDINE 348
Db 346 ASTSPTQSLVDSQAS-----KTLPI-----PTSAPVALSSTGKP-----VLDAGP 386
QY 349 HLPWMIYFLLLVLVIV-----VGSIRKSSRTLKKG-----PRODPSAIVEKAGLKK 397
Db 387 VLEWVI-----LVVVVVGSSAFLLCHRRACRRIRQKHLHCYPVQTSQPKLELVDSRPR 441
QY 398 MPTQNRKWIYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASEREVAFAFNGYTTADHE 457
Db 442 RSTQLRS-----GASVTEPVAEERGLMSQPLME-TC-----HS 474
QY 458 RAYAAALQHWITR-----GPEASLAQLISALROHRRNDVVEKIRGLMEDTTOLETKLAL 511
Db 475 VGAAYLESPLQDASPAGGSPRDLPEPRVSTEHTNNKIEKIYIMKADTVIVGTVKAEL 534
QY 512 PMSPSPLSPSPIPSPNAKLENSALLAVEPSPQDNKGFFVDESEPL 558
Db 535 PEGRGLAGPAE-PELEEELE-----ADHTPHYPEQETEPEPL 569

```

Search completed: July 11, 2003, 15:49:32
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:47:23 ; Search time 25 Seconds
(without alignments)
1086.680 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 3456

Sequence: 1 MGTPSPSSALASCRIARR.....SQEASQTLDSVYSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3456	100.0	655	TR21_HUMAN	O75509 homo sapien
2	3059	88.5	655	TR21_MOUSE	Q9epu5 mus musculus
3	343.5	9.9	461	TR1B_HUMAN	P20333 homo sapien
4	304.5	8.8	401	T11B_RAT	O08727 rattus norv
5	301.5	8.7	401	T11B_HUMAN	O00300 homo sapien
6	301.5	8.7	401	T11B_MOUSE	O08712 mus musculus
7	287	8.3	300	TR6B_HUMAN	O95407 homo sapien
8	273.5	7.9	474	TR1B_MOUSE	P25119 mus musculus
9	238	6.9	415	TRR3_MOUSE	P50284 mus musculus
10	236.5	6.8	416	TR16_CHICK	P18519 gallus gall
11	235.5	6.8	255	TNR9_HUMAN	O07011 homo sapien
12	233	6.7	289	TNR5_MOUSE	P27512 mus musculus
13	228.5	6.6	435	TNR3_HUMAN	P36941 homo sapien
14	227	6.6	269	TNR5_BOVIN	Q28203 bos taurus
15	218.5	6.3	326	V72_MYXVL	P29825 myxoma viru
16	215.5	6.2	351	CRMB_COMPX	O73559 cowpo viru
17	211.5	6.1	325	V72_SFVKA	P25943 shope fibro
18	211.5	6.1	425	TR16_RAT	P07174 rattus norv
19	210.5	6.1	427	TR16_HUMAN	P08138 homo sapien
20	208.5	6.0	349	CRMB_CAMPS	Q8uay7 camelopox vi
21	206.5	6.0	349	CRMB_VARV	P34015 variola vir
22	206	6.0	625	TR11_MOUSE	O35305 mus musculus
23	205.5	5.9	616	TR11_HUMAN	Q9y6q6 homo sapien
24	205	5.9	283	TR14_HUMAN	O92956 homo sapien
25	205	5.9	595	TNR8_HUMAN	P28908 homo sapien
26	200	5.8	277	TNR5_HUMAN	P25942 homo sapien
27	199.5	5.8	417	TR16_MOUSE	Q920w1 mus musculus
28	195	5.6	471	TR16_BOVIN	O19131 bos taurus
29	193	5.6	461	TR1A_PIG	P50555 sus scrofa
30	187.5	5.4	493	TNR8_RAT	P97525 rattus norv
31	186.5	5.4	461	TR1A_RAT	P22934 rattus norv
32	180.5	5.2	256	TNR9_MOUSE	P20334 mus musculus
33	176	5.1	498	TRR8_MOUSE	Q60846 mus musculus

RESULT 1

ID	TR21_HUMAN	STANDARD:	PRT:	655 AA.
AC	O75509; Q96D86;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-DE related death receptor-6) (Death receptor 6).			
GN	TNFRSF21 OR DR6.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98378343; PubMed=9714541;			
RA	Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.;			
RT	"Identification and functional characterization of DR6, a novel death domain-containing TNF receptor.";			
RL	FEBS Lett. 431:351-356(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Parker A.;			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Colon;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.			
CC	-!- SUBUNIT: Associates with TRADD.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).			
CC	-!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.			
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.			
CC	-----			
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CC	-----			
DR	EMBL; AF068868; AAC34583.1; -			
DR	EMBL; AL096801; CAB75692.1; -			
DR	EMBL; BC017730; AAH17730.1; -			
DR	EMBL; BC10241; AAH10241.1; ALT_INIT.			
DR	Genew; HGNC:13469; TNFRSF21.			

34	175	5.1	176	1	TR23_MOUSE	Q9er63 mus musculus
35	170	4.9	454	1	TR1A_MOUSE	P25118 mus musculus
36	162	4.7	259	1	T10C_HUMAN	O14798 h tumor nec
37	154	4.5	277	1	TNR4_HUMAN	P43489 homo sapien
38	149.5	4.3	1193	1	LMG2_HUMAN	Q13753 homo sapien
39	148	4.3	271	1	TNR4_RAT	P15725 rattus norv
40	146	4.2	180	1	TR22_MOUSE	Q9er62 mus musculus
41	145.5	4.2	455	1	TR1A_HUMAN	P19438 homo sapien
42	142	4.1	417	1	TR12_HUMAN	Q93038 h tumor nec
43	136	3.9	272	1	TNR4_MOUSE	P47741 mus musculus
44	135.5	3.9	5376	1	ZAN_MOUSE	O88799 mus musculus
45	131.5	3.8	440	1	T10B_HUMAN	O14763 homo sapien

ALIGNMENTS

```
DR MTM; 605732; -.
DR HSP; O14763; 1D0G.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT DOMAIN 42 349
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 50 88
FT REPEAT 90 131
FT REPEAT 133 167
FT REPEAT 170 211
FT DISULFID 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
FT CARBOHYD 82 82
FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 278
FT CARBOHYD 289 289
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 100.0%; Score 3456; DB 1; Length 655;
Best Local Similarity 100.0%; Pred. No. 9..8e-220;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATMTIAGSLLLGLFTTTAQPQKASNLIGTYRHVDRA 60
DB 1 MGTSPSSSTALASCSRIARRATMTIAGSLLLGLFTTTAQPQKASNLIGTYRHVDRA 60

QY 61 TGOVLTCDCPCAGTYVYSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCWPWIEK 120
DB 61 TGOVLTCDCPCAGTYVYSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCWPWIEK 120

QY 121 LPCAALTDRECTCPGCFMFSNATCAPHTVCPVGWGVKKGTETEDVRCKQCARGTSDVP 180
DB 121 LPCAALTDRECTCPGCFMFSNATCAPHTVCPVGWGVKKGTETEDVRCKQCARGTSDVP 180

QY 181 SSVMKCKAYTDCLSQNLVVKPCTKETDNVCGTLPFSFSSSTSPSPGTAIFPRPEHMETHE 240
DB 181 SSVMKCKAYTDCLSQNLVVKPCTKETDNVCGTLPFSFSSSTSPSPGTAIFPRPEHMETHE 240

QY 241 VPSSTVYVPGMNSTESNSASVRPKVLSIQEQTVPDNTSSARGKEDVAKTLPNLQVNH 300
DB 241 VPSSTVYVPGMNSTESNSASVRPKVLSIQEQTVPDNTSSARGKEDVAKTLPNLQVNH 300

QY 301 QOGPHRHILKLLPSMEATGGEKSTPIKGRKGRHPRQNLKHFDNEHLPWMVIFLL 360
DB 301 QOGPHRHILKLLPSMEATGGEKSTPIKGRKGRHPRQNLKHFDNEHLPWMVIFLL 360

QY 361 VLWVIVVCSIRKSRRLTKKGRQDPSAIVEKAGLKKSMPTQNREKWIYVCNGHGDI 420
DB 361 VLWVIVVCSIRKSRRLTKKGRQDPSAIVEKAGLKKSMPTQNREKWIYVCNGHGDI 420
```

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QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTADHERAYAAQLQHWITRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTADHERAYAAQLQHWITRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTTQLETDKALPNSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTTQLETDKALPNSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540

QY 541 SPQDNKNGFFVDESEPLLCDCSTSSGSSSALSRNGSFITTEKKTQVLRQVRLDPCDLQPIF 600
DB 541 SPQDNKNGFFVDESEPLLCDCSTSSGSSSALSRNGSFITTEKKTQVLRQVRLDPCDLQPIF 600

QY 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLLDSVYSHLPDLL 655
DB 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLLDSVYSHLPDLL 655

RESULT 2
TR21_MOUSE STANDARD; PRT; 655 AA.
AC Q9EPU5; Q9LXH9; Q9LW77;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chordata; Sciuromorphia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-x., Wang X., Cal Z.;
RT "Murine DR6: murine TNFR-related death receptor-6.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION
RX MEDLINE=21571606; PubMed=11714751;
RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal kinase activity and T cell
RT differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448(2001).
CC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC similarity). May activate JNK and be involved in T-cell
CC differentiation.
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC May be involved in T-cell differentiation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC thymus, testis, prostate, ovary, small intestine, colon, brain,
CC lung and kidney, and in fetal brain, liver and lung. Detected at
CC lower levels in adult peripheral blood leukocytes, lung, and in
CC fetal muscle, heart, kidney, small intestine and skin. Detected in
CC T-cells, B-cells and monocytes. In T-cells expression is highest
CC in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
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CC DR EMBL; AF322069; AAG38115.1; -
 CC DR EMBL; AY043489; AAK74193.1; -
 CC DR EMBL; BC016420; AAH16420.1; -
 CC DR HSSP; O14763; ID0G.
 CC DR MGD; MGI:2151075; Tnfrsf21.
 CC DR InterPro; IPR000488; Death.
 CC DR InterPro; IPR001368; TNFR_c6.
 CC DR Pfam; PF00020; TNFR_c6; 4.
 CC DR ProDom; PD000771; TNFR_c6; 1.
 CC DR SMART; SM00005; DEATH; 1.
 CC DR SMART; SM00208; TNFR; 4.
 CC DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 CC DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 CC DR PROSITE; PS00500; TNFR_NGFR_2; 1.
 CC KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 CC FT SIGNAL 1 41
 CC FT CHAIN 42 655
 CC FT
 CC FT DOMAIN 42 349
 CC FT TRANSMEM 350 370
 CC FT DOMAIN 371 655
 CC FT DOMAIN 415 498
 CC FT REPEAT 50 88
 CC FT REPEAT 133 167
 CC FT REPEAT 170 211
 CC FT REPEAT 67 80
 CC FT DISULFID 70 88
 CC FT DISULFID 91 106
 CC FT DISULFID 109 123
 CC FT DISULFID 113 131
 CC FT DISULFID 133 144
 CC FT DISULFID 150 168
 CC FT DISULFID 171 186
 CC FT DISULFID 192 211
 CC FT CARBOHYD 82 82
 CC FT CARBOHYD 141 141
 CC FT CARBOHYD 252 252
 CC FT CARBOHYD 257 257
 CC FT CARBOHYD 278 289
 CC FT CARBOHYD 289 289
 CC FT CONFLICT 352 352
 CC FT CONFLICT 523 523
 CC SQ SEQUENCE 655 AA; 71982 MW; 58C7C51C7C99EFF7 CRC64;
 Query Match 88.5%; Score 3059; DB 1; Length 655;
 Best Local Similarity 88.9%; Pred. No. 1.2e-193;
 Matches 583; Conservative 19; Mismatches 52; Indels 2; Gaps 2;
 QY 1 MGTSPSSALASCRIARRATATMIAGSLLLGLSTTTTAQPEKASNLGTVRHVDRA 60
 DB 1 MGRASSITALASCISRTAGQVATWAGSLLLGLSTTTTAQPEKTLSPGTVRHVDRT 60
 QY 61 TGOVLTCDCPAGTVVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCPCPCWPMTEK 120
 DB 61 TGOVLTCDCPAGTVVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCPCPCWPMTEK 120
 QY 121 LPCAALTDRECTCPGMPQSNATCAPHTVCVPVGVGVRKKGTETEDVRCCKQCARGTFSVP 180
 DB 121 LPCAALTDRECTCPGMPQSNATCAPHTVCVPVGVGVRKKGTETEDVRCCKQCARGTFSVP 180
 QY 181 SSVMKCKAYTDCLSQNLVWIKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPRPEHMETHE 240
 DB 181 SSVMKCKAHTDCLGONLEWVRKPGTKETDNVCGMLFFSSTNPPSPSGTVTFSHPEHMETHE 240

QY 241 VPSSTYVPKGMNSTESSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPLNQVNH 300
 DB 241 VPSSTYEPQGMNSTDSNSTASVTKVPFSGIEEGTVPDNTSSTSCKECTNRTLPNPQVTH 300
 QY 301 QQGPHHRIKLKLP-SWEATGGKSSPTPKGPKRGHPRONKHFDINEHLPWMIVLFL 359
 DB 301 QQAPHHRIKLKLPSSMEAT-GEKSSAIKAPKRGHPRONAHKHFIDINEHLPWMIVLFL 359
 QY 360 LVLVIVVVCSTRKSSRTLKKGPRODPSAIVKAGLKKSMPTQNRKWIYCNHGHDIL 419
 DB 360 LVLVIVVCSIRKSSRTLKKGPRODPSAIVKAGLKKSLTPTQNRKWIYRNHGHDIL 419
 QY 420 KLVAAGVGSQWKDIYQFLCNASEREVAAFNGYTDHERAYAAALQHTWTIRGPEASLAQL 479
 DB 420 KLVAAGVGSQWKDIYQFLCNASEREVAAFNGYTDHERAYAAALQHTWTIRGPEASLAQL 479
 QY 480 SALRQHRNDVVEKIRGLMEDTTQETDKKALPMSPSPPLSPSPSPNAKLENSALITVE 539
 DB 480 SALRQHRNDVVEKIRGLMEDTTQETDKKALPMSPSPPLSPSPSPNAKLENSALITVE 539
 QY 540 PSPODKNGKGFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKDTVLQVRLDPCDLQPI 599
 DB 540 PSPLDKNGKGFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKDTVLQVRLDPCDLQPI 599
 QY 600 FDDMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSVSHLPDLL 655
 DB 600 FDDMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSVSHLPDLL 655
 RESULT 3
 TR1B_HUMAN STANDARD; PRT; 461 AA.
 ID AC P2033; O16042;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
 DE [Contains: Tumor necrosis factor binding protein 2 (TNFII)].
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RA "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RT Science 248:1019-1023(1990).
 RL [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96299745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE OF 37-461 FROM N.A.
 RX MEDLINE=91370690; PubMed=1966549;
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,

RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RN Cytokine 2:231-237(1990).
RN [5]
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE-90349572; PubMed-2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [6]
RP SEQUENCE OF 27-31.
RX MEDLINE-90110215; PubMed-2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RT J. Biol. Chem. 265:1531-1536(1990).
RN [7]
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE-91056048; PubMed-2173696;
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RT J. Biol. Chem. 265:20131-20138(1990).
RN [8]
RP CHARACTERIZATION.
RX MEDLINE-93016040; PubMed-1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RT J. Biol. Chem. 267:21172-21178(1992).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP TRAF2.
RX MEDLINE-99221490; PubMed-10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2.";
RL Nature 398:533-538(1999).
CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFSF1/lymphotoxin-alpha.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -1- PTM: Phosphorylated; mainly on serine residues and with a very low
CC level on threonine residues.
CC -1- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC produced from the membrane form by proteolytic processing.
CC -1- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC Wyeth-Lyerst). Used to treat moderate to severe rheumatoid
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
CC TNF-alpha and blocks its interactions with receptors.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".
CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC WWW="http://www.enbrelinfo.com/".
CC -----
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CC -----
CC EMBL; M32315; AAA59929.1; -.

DR EMBL; U52165; AAC50622.1; -.
DR EMBL; U52156; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAA36755.1; -.
DR EMBL; S63368; AAB19824.2; -.
DR EMBL; M35857; AAA63262.1; -.
DR PIR; A35356; A35356.
DR PIR; A36007; A36007.
DR PIR; A36475; A36475.
DR PIR; B35010; B35010.
DR PIR; A23666; A23666.
DR PDB; 1CA9; 12-APR-99.
DR Genew; HGNC:11917; TNFRSF1B.
DR MIM; 191191; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Phosphorylation; Pharmaceutical; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR
FT CHAIN 27 461 SUPERFAMILY MEMBER 1B, MEMBRANE FORM.
FT DOMAIN 23 257 TUMOR NECROSIS FACTOR BINDING PROTEIN 2.
FT TRANSMEM 258 287 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 288 461 POTENTIAL.
FT REPEAT 39 76 CYTOPLASMIC (POTENTIAL).
FT REPEAT 77 118 TNFR-CYS 1.
FT REPEAT 119 162 TNFR-CYS 2.
FT REPEAT 171 201 TNFR-CYS 3.
FT REPEAT 201 233 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 141 141 R -> P (IN REF. 5).
FT CONFLICT 196 196 M -> R (IN REF. 2 AND 5).
FT CONFLICT 363 363 A -> T (IN REF. 5).
SQ SEQUENCE 461 AA; 48291 MW; 603D0AE1CD69ACBF CRC64;
Query Match 9.9%; Score 343.5; DB 1; Length 461;
Best Local Similarity 29.2%; Pred.No.1.9e-15;
Matches 95; Conservative 35; Mismatches 116; Indels 79; Gaps 11;
QY 65 LPTCDKCPAGTYVSEHCNTNTSLRVCSQCPVGTTRHENGIEKCHDCSQCPQPMWIEKLPCA 124
DB 52 MCCSKCSPQAKHAKVCTKTSTDFVDCSDSTVTLWNVPECLSCGSCSSDQVETQACT 111
QY 125 ALTDRETCPPGNF-----QSNATCAPHTVCPGVGVKKGKTETEDVRCOKARGTFSD 178
DB 112 RQNRICRCPGVCALSKQECRCPLKRCRPGFVGARPGTETSDVYVKPCAPGTFEN 171
QY 179 VPSSVMKCKAYTDCLSQNLVWIKPTGTETDNNVCGTLPSSFSSSTSP-----SPGTALFFPRP- 233
DB 172 TTSSSDICRPHQIC---NVVAI-PGNASMDAVC-----TSTSTPSRMAPGAVHLPPV 220


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Oy . 234 -----EHMETHEVPS-----STYVPGKMNSTESNS----- 259
Db 221 STRSQHTQPTPEPSTAPSTFLLPMGPSPPAEGSTGDFALPVLGVGTALGLLLIGVWN 280
Oy 260 -----ASVRPKVLSSIOGTPVD-NYSSARGKEDVKNKTLPLNLOVNVHQQGPHRRHILKLP 314
Db 281 CVIMTQVKKKPLCLQREAKVPHLPADKARG-----TOGPEQOHLITAP 324
Oy 315 SMEATGGKESSTPT--KGPKRGHPR 337
Db 325 SSSSSLESSASALDRAPTRNQPO 349

RESULT 4
T11B_RAT
ID T11B_RAT STANDARD; PRT; 401 AA.
AC O0872;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- INDUCTION: Upregulated by osteopontin.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC -----
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CC -----
DR EMBL; U94330; AAB53707.1; -
DR HSSP; P25942; 1CDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.

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FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
SQ SEQUENCE 401 AA; 46192 MW; 46192 MW; FEC6A31FID4E573A CRC64;

Query Match 8.8%; Score 304.5; DB 1; Length 401;
Best Local Similarity 28.6%; Pred. No. 5.8e-13;
Matches 91; Conservative 44; Mismatches 142; Indels 41; Gaps 9;

Oy 30 LLLGLSTTTAQ--PEKASNLIGTYRHVDRTGQVLTCDKCPAGTYVSHCHTNSLRV 87
Db 10 LVFLDIIEWTTFETFPK-----YLHYDPTGTQLLCKDKCAPGYLKQCHVRRKTL 61
Oy 88 CSSCPVCTFFRHENGIEKHCDCSQCPWPMEKLPKCAALTDRECTCPGMEQSNATCAPH 147
Db 62 CVPCPDYSYDTSWHTSDCEVYCSVCKELQTVQKCEKTRHNRVCEGGRLEFCLKH 121
Oy 148 TVCPGVGVRKKGKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVYIKPGTKET 207
Db 122 RSCPPGLGVLAGTGPRTNVCVKRCPDGFSGSETSKAPCRKHTNCSSLLGLLIQGNATH 181
Oy 208 DNVCGTLPSSSTSPSPGTAIFRPRHEMETHVPSTTYVPKGMN-----STESNSA 260
Db 182 DNVG-----SGNREATCGIDVTLCCEAFFRFAVPTK-IIPNWLSQLVDSLPGTKVNAES 236
Oy 261 SVRPKVLSSIOGTPV-----DNTSSARGKEDVKNKTLPLNLOVNVHQQGPHRRHI----- 309
Db 237 VERIKRRHSSQEQTFQLLKLKHKHON-----RDQEMVKLIQDIDLCSSVQRHGHANLTT 292
Oy 310 --LKLPSMEATGKES 325
Db 293 EQLRIL--MESLPCKKIS 308

RESULT 5
T11B_HUMAN
ID T11B_HUMAN STANDARD; PRT; 401 AA.
AC O00300; O60236; Q9UHP4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,

```

RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombo A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=942069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RX Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor";
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN [6]
RP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RX He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens";
RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN [7]
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977;
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis";
RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN [8]
RP TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Dean K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dadds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL";
RL J. Biol. Chem. 273:14363-14367(1998).
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.;
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor";
RL J. Biol. Chem. 273:5117-5123(1998).
RN [10]
RP REVIEW.
RX MEDLINE=21395914; PubMed=11505389;

RA Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases";
RL Cancer 92:460-470(2001).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC lymph node, trachea, adrenal gland, testis, and bone marrow.
CC Detected at very low levels in brain, placenta and skeletal
CC muscle. Highly expressed in fetal kidney, liver and lung.
CC -!- INDUCTION: Upregulated by increasing calcium-concentration in the
CC medium and estrogens. Downregulated by glucocorticoids.
CC -!- PTM: N-glycosylated. Contains sialic acid residues.
CC -!- PTM: N-terminus may be blocked.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U94332; AAB53709.1; -;
CC EMBL: AB002146; BAA25910.1; -;
CC EMBL: AB008822; BAA32076.1; -;
CC EMBL: AB008821; BAA32076.1; JOINED.
CC EMBL: BC030155; AAB30155.1; -;
CC EMBL: AF134187; AAF20168.1; -;
CC HSSP: P25942; ICDF.
CC Genew: HGNC:11909; TNFRSF11B.
CC MIM: 602643; -;
CC InterPro: IPR000488; Death.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 3.
CC ProDom: PD000771; TNFR_c6; 1.
CC SMART: SM00005; DEATH; 1.
CC SMART: SM00208; TNFR; 4.
CC PROSITE: PS00017; DEATH_DOMAIN; FALSE_NEG.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00650; TNFR_NGFR_2; 2.
CC Receptor: Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
CC SIGNAL 1 21
CC CHAIN 22 401
CC TUMOR NECROSIS FACTOR RECEPTOR
CC SUPERFAMILY MEMBER 11B.
CC REPEAT 24 62
CC TNFR-CYS 1.
CC REPEAT 65 105
CC TNFR-CYS 2.
CC REPEAT 107 142
CC TNFR-CYS 3.
CC REPEAT 145 185
CC TNFR-CYS 4.
CC DOMAIN 198 269
CC DEATH 1.
CC DOMAIN 270 365
CC INVOLVED IN DIMERIZATION.
CC SITE 400 400
CC BY SIMILARITY.
CC DISULFID 41 54
CC BY SIMILARITY.
CC DISULFID 44 62
CC BY SIMILARITY.
CC DISULFID 65 80
CC BY SIMILARITY.
CC DISULFID 83 97
CC BY SIMILARITY.
CC DISULFID 87 105
CC BY SIMILARITY.
CC DISULFID 107 118
CC BY SIMILARITY.
CC DISULFID 124 142
CC BY SIMILARITY.
CC DISULFID 145 160
CC BY SIMILARITY.
CC DISULFID 166 185
CC BY SIMILARITY.
CC CARBOHYD 98
CC N-LINKED (GLCNAC...) (POTENTIAL).

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FT CARBOHYD 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 3 K -> N.
FT /FTid=VAR_013439.
FT MUTAGEN 400 C->S: ABOLISHES DIMERIZATION.
FT MUTAGEN 400 MISSING: ABOLISHES DIMERIZATION.
FT CONFLICT 263 D -> A (IN REF. 1).
SQ SEQUENCE 401 AA; 46040 MW; EDF448B67D86C71E CRC64;

Query Match 8.7%; Score 301.5; DB 1; Length 401;
Best Local Similarity 24.8%; Pred. No. 9.1e-13;
Matches 102; Conservative 58; Mismatches 177; Indels 75; Gaps 13;

Qy 54 YRHVDRTGQVLTCDKCPAGTVYSEHTNTSLRYVCSGPCVGTFRHENGLEKCHDCSQPC 113
Db 28 YLHVDERTSHQLLCKDPPGYLQKHTAKWTVCAFCPDHYHDTSDWHTSDECLYCSVC 87

Qy 114 PPMIEKLPCALTDRECTCPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCAR 173
Db 88 KELQVQECNRTHNRVCECKEGRYLETFCLKHRSCPPGGVGVQAGTPERNVTCKRCPD 147

Qy 174 GTFSDVPSSVNMCKAYTCLSONLVKPKGTEDNVCGLTLPFSSTSPSPGTAIPRP 233
Db 148 GFFSNETSSKAPCRKHTNCVSFGLLTQKGNATHDNC-----SGNSESTQKCGIDVTLC 203

Qy 234 EHMETHEVPSYVYPKGMN-----STESNSSASVRPKVLSLQIEGTVP-----DNT 279
Db 204 EAFRFVPTK-FPNWLSVLVDNLPGTKVNAESVERIKRQHSQEQTFQLLKWKQN- 261

Qy 280 SSARGKEDVNTLPNLQVNHQGFPHRH-----ILKLLPSMEATGKESSTPIK 329
Db 262 ---KQDQIVKIIQIDILCENSQVRHIGHANLTPEQLRSLMESLPG-KKVGAEDIEKTIK 317

Qy 330 GPKRGHPQNLKHFIDNEHLPWMLVLELLVLVIVVVCSTRKSRILKKGPRQDPSAIV 389
Db 318 ACK---PSDQILKLLSL---WRI-----KNGDQDTLKLGLM 346

Qy 390 EKAGLKKS-----MTPTQNKRWIYVYCNHGIDIL--KLVAAGVGSQWKDI 433
Db 347 H--ALKHSKTHFFKTVTQSLKKTKIRFLHSFTMYKLQKLFLEMIGNOVQSV 396

RESULT 6
T11B_MOUSE
ID T11B_MOUSE STANDARD; PRT; 401 AA.
AC 008712; 070202;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPB OR OCIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288

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RP AND ARG-296.
RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
RN [3]
RP FUNCTION.
RX MEDLINE=21060987; PubMed=10952716;
RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA Simonet W.S.;
RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT osteoclasts and prevents vascular calcification by blocking a process
RT resembling osteoclastogenesis.";
RL J. Exp. Med. 192:463-474(2000).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC intestines and calvaria. Highly expressed in decidua and placenta,
CC and in embryo.
CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
CC whereas expression decreases at day 11 and increases from day 15
CC to 17. On day 15' found in developing bone primordia,
CC brachiocephalic artery and ductus arteriosus, left main bronchus,
CC abdominal aorta and midgut.
CC -!- INDUCTION: Upregulated by IGF-beta and estrogens. Downregulated by
CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U94331; AAB53708.1; -
DR EMBL; AB013898; BAA28269.1; -
DR EMBL; AB013903; BAA33388.1; -
DR EMBL; AB013899; BAA33388.1; JOINED.
DR EMBL; AB013900; BAA33388.1; JOINED.
DR EMBL; AB013901; BAA33388.1; JOINED.
DR EMBL; AB013902; BAA33388.1; JOINED.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:109587; Tnfrsf11b.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS06552; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR
FT REPEAT 24 62 TNFR-CYS 1.
FT REPEAT 65 105 TNFR-CYS 2.
FT REPEAT 107 142 TNFR-CYS 3.

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FT REPEAT 145 185 TNFR-CYS 4.
FT DOMAIN 198 269 DEATH 1.
FT SITE 283 365 INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT DISULFID 40 400 BY SIMILARITY.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT DISULFID 166 185 BY SIMILARITY.
FT CARBOHYD 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH
FT VARIANT 161 161 SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH
FT VARIANT 165 165 SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH
FT VARIANT 296 296 SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 8.7%; Score 301.5; DB 1; Length 401;
Best Local Similarity 29.0%; Pred. No. 9.1e-13;
Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;

QY 30 LLLGLSLTSTAPEQKASNLIGTYRHVDRAITGCDKCPAGTVVSEHCTWTSLRVCS 89
DB 10 LVLLDIETWTE-----TLPKYLHYDPETGCHQLLCKDCAPGTLYKHCTVRRRTLCV 63
QY 90 SCPVGTFTTHRENGIEKCHDCQPCPWPMTIEKLPCAALTIRECTCPGPMFSNATCAPHTV 149
DB 64 PCPDHSYTDWHTSDCEVYCSVCKELQSVKQECNTHNRVCEBGRVLETEFLCKHRS 123
QY 150 CPVGWVRKKGTEDEVCKCARGTFSDVPSSVMCKAYTDCLSNLVIVIRPGTKETDN 209
DB 124 CPPGSGVAGVGPETNVTCKKCDGFGSETSKAPCIKHNTCTFGLLLIQKGNATHDN 183
QY 210 VCTLPFSSTSPSPGTAIFRPEHMETHEVPSSTYVPKGMN-----STESNSSASV 262
DB 184 VC-----SGNREATQKCGIDVTLCEEAFFRAVPTK-IIPNLSVLVDLPGTKVNAESVE 238
QY 263 RPKVLSIOEGTVP-----DNTSSARGKEDVKNLPLQVNVHQQGPHHRH-----ILK 311
DB 239 RIKRRHSSQEQTFQLLKLKHQN-----RDQEMVKKIQTIDLCSSVQRHLGHSNLTTEQ 294
QY 312 LLPSMEATGEKSS 325
DB 295 LLALMESLPKKIS 308

RESULT 7
TR6B_HUMAN
ID TR6B_HUMAN STANDARD; PRT; 300 AA.
AC Q95407;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (Dcr3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Submitted R.;
RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL Submitter: Decoy receptor for the cytotoxic ligands TNFSF4/LIGHT
CC and TNFSF6/FasL. Protects against apoptosis.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
CC Detected in adult stomach, spinal cord, lymph node, trachea, tumors
CC spleen, colon and lung. Highly expressed in several primary tumors
CC from colon, stomach, rectum, esophagus and in SW480 colon
CC carcinoma cells.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF104419; AAD03056.1; -
CC EMBL: AF134240; AAD29688.1; -
CC EMBL: AF217796; AAF35244.1; -
CC EMBL: AF217793; AAF33685.1; -
CC EMBL: AF217794; AAF33686.1; -
CC EMBL: AL121845; CAC03668.1; -
CC EMBL: BC017065; AAH17065.1; -
CC Genew; HGNC:11921; TNFRSF6B.
CC MIM; 603361; -
CC HSP; O14763; ID0G.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 4.
CC ProDom: PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00505; TNFR_NGFR_2; 2.
KW Receptor; apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 29
```


Db 209 LSAIPRTLYVSQPEPTRSRPLDQEPGSPQTPSILTSL--GSTPIIEQSTKG-----GISLP 262
QY 294 -----NLQVW-----HQQPH-----HRHLK 311
Db 263 IGLIVGVTSLGLMLGLVNCILIVQRKKPSCILORDAKVPHVPDEKSDQAVGLEQQHLIT 322
QY 312 LPSMBATGGEKSST--PIKPKRGHPR 337
Db 323 TAPSSSSSSLESSASAGDRRAPGGHPQ 350
RESULT 9
TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (lymphotoxin-beta receptor).
GN LTBR OR TNFRSF3 OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.D., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: Isolation by the signal
RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs
CC (By similarity).
CC -!- SUBUNIT: Self-associates (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U29173; AAC68964.1; -
DR EMBL: L38423; AAB00846.1; -
DR EMBL: U30798; AAA81334.1; -
DR HSSP: O14763; ID0G.
DR MGD: MGI:104875; Ltbr.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 3.

FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 245 POTENTIAL.
FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 170 TNFR-CYS 3.
FT REPEAT 171 213 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;
Query Match 6.9%; Score 238; DB 1; Length 415;
Best Local Similarity 23.5%; Pred. No. 1.4e-08;
Matches 95; Conservative 40; Mismatches 144; Indels 126; Gaps 17;
QY 16 RIARRATATMIAGSLLLGLFLSTTTTAQPEQKASNLIGTYRHVDRA-----GQV 64
Db 2 RLPRASSPCGLAWGPLLLGLGLVASQPQ---LVPPYR-IEQTCWDQDKEYEYPMHD 56
QY 65 LTCDKCPAGTYSEHCTNTSLRVCSCPVGTFTTRHENGIEKHCDCSQCPWPM--TEKLP 122
Db 57 VCCSRCPGGEFVAVGSRSDQTVCKTTPHNSNEHWNHLSLTCQLC-RPCDIVLGFEVAP 115
QY 123 CAALTDRECTCPGPM---EQSN-----ATCAPHTVCPVGWGVKKGTE----- 164
Db 116 CTSDRKAECRCQGMSCVYLDNECVCEERLVLCOP-----GTAEVYDEI 162
QY 165 ---DVRCKQCARGTFSVPSSVMKKAYTDCLSQNLVVKPGTKETDNVCGTLPS----- 216
Db 163 MDTDVNCVCKPGHFQNTSSPRARCQPHTRCEIQLGLVEAAAGTSTYDICKNPPEGAML 222
QY 217 -----FSS-----STSPSGCTAIFPRPEHMETHEVSPSTVVPKGMNS 253
Db 223 LLAILLSLVLLFTTTLACAMMRHPSLCRKLKRLHREGESEPPCPAPRADPH----- 278
QY 254 TESNSASVRPKVLSIIQGTVP---DNTSSARGKEDVANKTLPNL-QVYNHQGP----- 304
Db 279 -----FPDLAEPLPMSGDLSPSPAGP---PTAPSLSEVVLQQSPLVQAR 321
QY 305 -----HHRHLKLLPSMEATGGEKSST-----PIKPKRG 334
Db 322 ELEAEPEGHQVAHGANGIHVTGGSVTVGTNIYNGPVLGGTRG 366
RESULT 10
TNR16_CHICK STANDARD; PRT; 416 AA.
AC P18519;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RX MEDLINE=90166579; PubMed=2560385;
RA Large T.H., Weskamp G., Heider J.C., Radeke M.J., Misko T.P.,
RA Shooter E.M., Reichardt L.F.;
RT "Structure and developmental expression of the nerve growth factor
RT receptor in the chicken central nervous system.";
RL Neuron 2:1123-1134(1989).
RN [2]
RP SEQUENCE OF 21-416 FROM N.A.
RX MEDLINE=90152140; PubMed=2154393;
RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
RT "Structure and developmental expression of the chicken NGF receptor.";
RL Dev. Biol. 137:287-304(1990).
CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC and NT-4. Can mediate cell survival as well as cell death of
CC neural cells (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC associated cell death executor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: N- AND O-glycosylated.
CC -!- PTM: Phosphorylated on serine residues.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DR PIR; JN0006; JN0006.
DR PIR; A60504; A60504.
DR HSP; P07174; INGR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; death; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Phosphorylation; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 416 TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 16.
FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 240 261 POTENTIAL.
FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).
FT REPEAT 23 57 TNFR-CYS 1.
FT REPEAT 58 99 TNFR-CYS 2.
FT REPEAT 100 138 TNFR-CYS 3.
FT REPEAT 140 180 TNFR-CYS 4.
FT DOMAIN 333 410 DEATH.
FT DOMAIN 188 236 SER/THR-RICH.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 36 36 C -> Y (IN REF. 2).
FT CONFLICT 173 173 T -> K (IN REF. 2).
FT CONFLICT 276 276 N -> S (IN REF. 2).
FT CONFLICT 396 396 K -> R (IN REF. 2).
SQ SEQUENCE 416 AA; 44654 MW; 6BCEAAB54F4D2D56 CRC64;
Query Match 6.8%; Score 236.5; DB 1; Length 416;
Best Local Similarity 23.2%; Pred. No. 1.8e-08;
Matches 105; Conservative 50; Mismatches 191; Indels 107; Gaps 15;
QY 67 CDKCPAGTYVSEHCTNLSRVCSHC-PVGTFTRHNGIEKHCDSQPCPWPMEIKLPCAA 125
| | | | | : | | | | | : | | | | |

Db 36 CKACNLGEGVQPC-GVNTQVCEPCLDSVTYSIDTVSATEPCKPCTQ-CVGLHSMSPCPE 93
QY 126 LTRECECTPPGMFQS--NATCAPIHTVCPVGWGRKKGTETEDVRCKOCARGTSDVPSSV 183
Db 94 SDAVACRCAYGYFQDELSGSCKECSICEVGFGLMFPDQSDIVCECPGEGTSDANFV 153
QY 184 MKCKAYTDCLSONLVIKPGTKETDNVCGTL-----PSFSSSTSPSPGTAIFPRPEH 235
Db 154 DPCLPCTIC-EENEVMVKECTATSDAECRLHPRWTTHTPSLAGSDSPETTRDPFNTG 212
QY 236 METHVEPSSIVYKGMNSTESNSAS-----VRPKVLSSIQEGIVPDNTSSARGEDVYNT 291
Db 213 MATTLADIVTVMGSSQPVVSRGTADNLIPVYCSILAAVVGVLVAYTAFKRWNSCKQKQ 272
QY 292 LPNLQVNVHGOOGPHRHILKLLPSMEATGKESSTPIKPKRGHPRONLKHKHEIDNEHLP 351
Db 273 GANNRPVNTQPSPE-----GEK-----LHSDSI----- 296
QY 352 WMIVLFLLLVIVVCSIRKSSRTLKGRQDPFSAIVEK--AGLKKSMPTTONREKIY 409
Db 297 -----SVDSQSLHDQPPNQSTQGPAPKDGSLYASLPPSKQEE----- 335
QY 410 YCNGHGIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFNSGY-----TADHERAYA 461
Db 336 -----VEKLLSSSAETWQL-----AGELGYKEDLIDCFTREESPARA 374
QY 462 ALQHWITRGPEASLAQLISALROHRRNDVVEKI 494
Db 375 LLADWSAK-ETATYLDALLVALRKIQORDIAESL 406
RESULT 11
TNFR_HUMAN
ID TNFR_HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
DE (CD137 antigen).
GN TNFRSF9 OR ILA OR CD137.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
PC TISSUE=Blood;
RA MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand.";
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RC SEQUENCE FROM N.A.
PC TISSUE=Blood;
RA MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family";
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RC SEQUENCE FROM N.A.
PC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,

FT	DOMAIN	31	227	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	228	248	POTENTIAL.
FT	DOMAIN	249	435	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	42	81	TNFR-CYS 1.
FT	REPEAT	82	124	TNFR-CYS 2.
FT	REPEAT	125	168	TNFR-CYS 3.
FT	REPEAT	169	211	TNFR-CYS 4.
FT	DISULFID	43	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	80	BY SIMILARITY.
FT	DISULFID	83	98	BY SIMILARITY.
FT	DISULFID	101	116	BY SIMILARITY.
FT	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	148	BY SIMILARITY.
FT	DISULFID	142	167	BY SIMILARITY.
FT	DISULFID	170	185	BY SIMILARITY.
FT	CARBOHYD	40	40	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	435 AA;	46709 MW;	624626E6022F656F CRC64;
Query Match				
Best Local Similarity 6.6%; Score 228.5; DB 1; Length 435;				
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;				
Qy	65	LTCDKCPAGYVVSSEHCTNTSLRVCSSCPVGTFTFRHENGIEKCHDCSOPC-PWPMIEKL-P	122	
Db	57	ICCSRCPPGYVSAKCSRIKRTVCATCAENSYNEHWNLYLTCQLC-RPCDPVVGLEBIAP	115	
Qy	123	CAALTDRETCPCPGMFOSNATCAPHTV-----CPVGMGVRKKGTETE-----	164	
Db	116	CTSKRKTKQCRCQPGMF-----CAWALECTHCELLSDCP-----PGTEALKDEVGKG	163	
Qy	165	DVRCKQCARCTESDPVSSVMKRAYTDCLSQNLVVIKPGTKETDNVCGT---LPSFSS	220	
Db	164	NNHCVPCKAGHFONTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTCKNPLELPPEMSG	223	
Qy	221	T 221		
Db	224	T 224		
RESULT 14				
TNRS_BOVIN				
ID	TNRS_BOVIN	STANDARD;	PRT;	269 AA.
AC	Q28203;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 5 precursor			
DE	(CD40L receptor) (B-cell surface antigen CD40) (fragment).			
GN	TNFRSF5 OR CD40			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
OC	Camellia; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=97281252; PubMed=91355560;			
RA	Hirano A., Brown W.C., Estes D.M.;			
RT	"Cloning, expression and biological function of the bovine CD40			
RT	homologue: role in B-lymphocyte growth and differentiation in			
RT	cattle."			
RL	Immunology 90:294-300(1997).			
CC	-1- FUNCTION: Receptor for TNFRSF5/CD40L.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:45:53 ; Search time 39 Seconds
(without alignments)

3460.535 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 3456

Sequence: 1 MGTSPSSSTALASCRIARR.....SQEASOTLLDSVYSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2356	68.2	651	13 Q98SM6	Q98sm6 gallus gall
2	453	13.1	132	13 Q90Y18	Q90y18 salvelinus
3	354	10.2	83	13 Q8UWJ0	Q8uwj0 gallus gall
4	308	8.9	285	13 Q90W71	Q90w71 oncorhynch
5	307	8.9	285	13 Q90X56	Q90x56 oncorhynch
6	275.5	8.0	433	13 Q91ZM6	Q91zm6 rattus norv
7	275.5	8.0	459	11 Q62327	Q62327 mus muscul
8	268.5	7.8	302	13 Q9PU50	Q9pus0 salvelinus
9	262.5	7.6	482	11 Q88734	Q88734 mus muscul
10	248.5	7.2	167	12 Q72762	Q72762 cowpox viru
11	248.5	7.2	167	12 Q8UYL3	Q8uyl3 vaccinia vi
12	240.5	7.0	167	12 Q9DJL2	Q9djl2 cowpox viru
13	238	6.9	351	12 Q57117	Q57117 cowpox viru
14	237.5	6.9	360	12 Q57118	Q57118 cowpox viru
15	233	6.7	351	12 Q57121	Q57121 cowpox viru
16	232.5	6.7	347	12 Q57119	Q57119 cowpox viru

17	231	6.7	277	6	Q8WMQ2	Q8wmq2 ovls arles
18	230.5	6.7	349	12	Q57100	Q57100 monkeypox v
19	230	6.7	348	12	Q57103	Q57103 monkeypox v
20	230	6.7	348	12	Q57108	Q57108 monkeypox v
21	230	6.7	348	12	Q57277	Q57277 monkeypox v
22	228.5	6.6	349	12	Q57102	Q57102 monkeypox v
23	228	6.6	347	12	Q57115	Q57115 cowpox viru
24	227.5	6.6	349	12	Q57101	Q57101 monkeypox v
25	227.5	6.6	349	12	Q57291	Q57291 monkeypox v
26	227	6.6	278	6	Q8SQ34	Q8sq34 sus scrofa
27	225.5	6.5	349	12	Q57099	Q57099 monkeypox v
28	225	6.5	355	12	Q85308	Q85308 cowpox viru
29	223.5	6.5	350	12	Q57116	Q57116 cowpox viru
30	221.5	6.4	349	12	Q57305	Q57305 cowpox viru
31	216.5	6.3	326	12	Q57120	Q57120 cowpox viru
32	215.5	6.2	351	12	Q73559	Q73559 cowpox viru
33	214.5	6.2	326	12	Q57122	Q57122 cowpox viru
34	212.5	6.1	350	12	Q57123	Q57123 cowpox viru
35	211.5	6.1	322	12	Q72761	Q72761 cowpox viru
36	208.5	6.0	349	12	Q57098	Q57098 camelpox vi
37	208.5	6.0	349	12	Q57109	Q57109 variola vir
38	208.5	6.0	349	12	Q8UYA7	Q8uya7 camelpox vi
39	208.5	6.0	349	12	Q57284	Q57284 camelpox vi
40	206.5	6.0	348	12	Q57112	Q57112 variola vir
41	206.5	6.0	348	12	Q85407	Q85407 variola vir
42	204.5	5.9	349	12	Q57110	Q57110 variola vir
43	204.5	5.9	349	12	Q57111	Q57111 variola vir
44	204.5	5.9	349	12	Q89098	Q89098 variola vir
45	204.5	5.9	349	12	Q89118	Q89118 variola vir

ALIGNMENTS

RESULT 1

Q98SM6 ID Q98SM6 PRELIMINARY: PRT; 651 AA.
 AC Q98SM6;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Death receptor 6.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bridgham J.T., Johnson A.L.;
 RT "Expression of DR6 in the ovary."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF349908; AAK29666.2; -
 DR HSSP; P19438; INCF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR003975; Shal_channel.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR PRINTS; PR01497; SHALCHANNEL.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 651 AA; 71003 MW; BDC95A60DAB2C2A CRC64;

Query Match 68.2%; Score 2356; DB 13; Length 651;

Best Local Similarity 70.8%; Pred. No. 1.2e-181; Indels 46; Gaps 10;
 Matches 470; Conservative 47; Mismatches 101;

QY 23 ATMTAGSLLLLGFLSTTTTAQP-----EQKASNL-ICTYRHVDRTATGQVLTCKCPAGTVYS 77

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Db 3 AAVLAAYLPLVLFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATNOELICDKCPAGTYVS 62
Qy 78 EHCNTSLRVSCSSCPVCTFTRHENGIEKCHDCSQPCPWPMEIKLPALCAALTDRECTCPGM 137
Db 63 KHCTKSTLRCSGPCDGTFTFHENGIBRCHPCRPCELPMEIKHTCHTALDRECTCLSGT 122
Qy 138 FQSNATCAPHTVCPVGVGVRKKGTEDETRCKOCARGTFSFSDVPSSVMKCKAYTDCLSONL 197
Db 123 FOINDTCVPTVCPVGVGVRKKGTEDETRCKPCLRGTFSDVPSSVMKCKTYDDCFKKNM 182
Qy 198 VWIKPGTKEDNVCG---TLP--SFSSSTSPSGCTAIFPRPEHMETHEVPSSTVYVPGKM 252
Db 183 VVYKPGTKESDNCVGSFASLPNTSLTSSDAQDQ-----ETVEAPPTAYLPKGLN 232
Qy 253 STESNSASVRPKVLSIQEGTVPDNTSSARGEDVKNKTLPLNQLVYVNHQGPGRHHLKL 312
Db 233 SSVFDLSSFPAPRVNGTAEPTVDYNDTSANGTVGAPGSLSSAGTAGQAQSYRKHHTSQ 292
Qy 313 L---PSMEATGGKSSPTIKPKRGHPRQNLKHFDINEHLPWMLVFLFLLVLVVIYVCS 369
Db 293 MGKQPAQEMAGGKSSIPYRPRRGP--NVHQHFDINEHLPWMLVFLFLLVLVVIYVCS 350
Qy 370 IRKSSRTLKKGPRQDSAIYVEKAGLKKSWPTQNRKWIYYCNGHGDIDILKLVAAQVGSQ 429
Db 351 VRKSSRTLKKGPRQDSAIYVEKAIMKSTTPTQNRKWIYYCNGHGDIDILKLVAAQVGSQ 410
Qy 430 WKDIYQFLCNASEREVAAFNGYTAHERAYAAALQHWITRGPEASLAQLISALRQHRND 489
Db 411 WKDIYQFLCNASEREVAAFNGYTAHERAYAAALQHWITRGPEASLAQLISALRQHRND 470
Qy 490 VVEKIRGLMEDTT-----QLETDKALPMSPLSPSPSPNAKLE 531
Db 471 VVEKIRGLMEDTTVPVQMOPQWQODCSNDGDKLEGDKLALPVSPSPSPVPTFSP--KPP 528
Qy 532 NSALLTVEPSQDNKNGFFVDESEPLLRCDSTSGSSALSRLNGSPFTKEKKTDLVLRQVRL 591
Db 529 DAAVLTVEPSSEK-KCFFVESEPLLRCDSTSGSSALSRLNGSPFTKEKKTDLVLRQVRL 587
Qy 592 DPCDLOPFDMLHFNPELRYEELPQAEKDLRLFEIIGVKSEFASOTLLDSVYSHL 651
Db 588 DPCDLOPFDMLHFNPELRYEELPQAEKDLRLFEIIGVKSEFASOTLLDSVYSHL 647
Qy 652 POLL 655
Db 648 POLL 651

RESULT 2
Q90Y18 PRELIMINARY; PRT; 132 AA.
AC Q90Y18;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Death receptor 6 (fragment).
GN DR6.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP BRIDGHAM J.T., BOBE J., GOETZ F.W., JOHNSON A.L.;
RT "Conservation of Death Receptor-6 (DR6) in avian and piscine
vertebrates.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2001).
DR EMBL; AF302499; AAL09310.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
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KW Receptor.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 14303 MW; B01FED44260C1E5 CRC64;

Query Match 13.1%; Score 453; DB 13; Length 132;
Best Local Similarity 56.1%; Pred. No. 6.3e-29;
Matches 74; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

Qy 74 TYVSEHCNTSLRVSCSSCPVCTFTRHENGIEKCHDCSQPCPWPMEIKLPALCAALTDRECTC 133
Db 1 TFVSRHCTQNVNDCSRCDGFTFHENGIEKCHDCSQPCPWPMEIKLPALCAALTDRECTC 60
Qy 134 PPGMFQSNATCAPHTVCPVGVGVRKKGTEDETRCKOCARGTFSFSDVPSSVMKCKAYTDCL 193
Db 61 PPDFTFGDSCSTAHSCLCPVGSVYKRGNDVEDVRCKACARGSFSDMASSVLKCTHTDCL 120
Qy 194 SQNLVVIKPGTK 205
Db 121 AQSLLPLAAGTR 132

RESULT 3
Q8UWJO PRELIMINARY; PRT; 83 AA.
AC Q8UWJO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Death receptor 6 (fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Shi Z., Onagbesan O.M., Williams J.;
RT "Apoptosis in chicken ovary";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432512; AAL35360.1; -.
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 83
SQ SEQUENCE 83 AA; 9506 MW; 28F8C880F655FADC CRC64;

Query Match 10.2%; Score 354; DB 13; Length 83;
Best Local Similarity 94.4%; Pred. No. 3.3e-21;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 434 YQFLCNASEREVAAFNGYTAHERAYAAALQHWITRGPEASLAQLISALRQHRNDVVEK 493
Db 1 YQFLCNASEREVAAFNGYTAHERAYAAALQHWITRGPEASLAQLISALRQHRNDVVEK 60
Qy 494 IRLGMDTTQLE 505
Db 61 IRLGMDTTQVQ 72

RESULT 4
Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


Query Match	8.0%	Score	275.5;	DB 11;	Length	459;			
Best Local Similarity	25.0%;	Pred.	No. 8e-14;						
Matches	82;	Conservative	34;	Mismatches	127;	Indels	85;	Gaps	10;

QY	65	LTCDKCPAGTYVSEHCTNTSLRVSSCPVCTFRHENGIEKCHDCSQCPWPMTLEKLP	CA 124
DB	38	MCCAKCPGGYVHKFKTSDTYCADCEASMYTVQVNFQTRCLSSCSSCTDQVETRACT	97
QY	125	ALTDRECTCPPGMFQSNAT-----CAPHTVCPVGMGRVKKGTETEDVRCKKOCARGTFS	177
DB	98	KQONRRVCAEAGRYCALKTHSGSCROCMRLSKCGPGFVASSRPNAGNVLCACAPGTF	157
QY	178	DVPSSVMKCKAYTDCLSQNLVTKPGTKETDNYCGTLPSFSSSTSPSPGTAIPRPBHE	237
DB	158	DTTSSDVCVRPHRIC-----SILAIPGNASTDAVCA-----PESPT	193
QY	238	THEVPSTTV-----PKGMNSTESNASVPPKVLSSIOEGTVPDNTSSARGKEDVNTLP	293
DB	194	LSAIPRTLVSQPEPTRSQPLDQPGPQSPSILTSL--GSTPIIEQSTKG---GHSLP	247
QY	294	-----NLQVNN-----HQQGPH-----HRRILK	311
DB	248	IGLIVGTVSIGLLMLGLVNCFILVQRKKKPSCLORDAKVPHVPEKXSQDAVGLQEQHLLT	307
QY	312	LLPSMEATGKESST--PTKGPKRGRHPR	337
DB	308	TAPSSSSSSLESSASAGDRRAPGGHPQ	335

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RESULT 8
Q9PUS0 PRELIMINARY; PRT; 302 AA.
ID
Q9PUS0;
AC Q9PUS0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
the brook trout (Salvelinus fontinalis) ovary at the completion of
ovulation."
RL Biol. Reprod. 62:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; ID4V.
DR InterPro; IPR001368; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ
SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 7.8%; Score 268.5; DB 13; Length 302;
Best Local Similarity 32.5%; Pred. No. 1.6e-13;
Matches 53; Conservative 26; Mismatches 81; Indels 3; Gaps 2;

QY 53 TYRHVDNRATGOVLTDCKCPAGTVVSEHCNTSLRVCGSSCPVGTFTRHENGIEKCHDCSQP 112
DB 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11:::
22 TPKNDDRYSGLSIVDCRCPGYLRAPCSAMRKSACAECPCNAYTEFWNHISKLRCSM- 80
QY 113 CPWPMTIEKLPALALTDRECTCPGME--QSNATCAPIHTVCPVGWGVKKGTETEDVRCKQ 170
DB 1::: 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11:::
81 CAENQVVKQECSPSNCECEKGEYFNKKYEACIKKKECPGYGANTTGTPHQDTECVQ 140
QY 171 CARGFTSDVPSSVMKCKAYTDCLSQNLVVIKPGTETDNCVT 213
DB 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11::: 11:::
141 COAGFYSEVSSAKATCLAOSNCKVGLRLVLRGQDWHHTLCAS 183

RESULT 9
O88734 PRELIMINARY; PRT; 482 AA.
ID
O88734;
AC O88734;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P80 TNF-alpha receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=98414512; PubMed=9740674;
RA Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
and Characterization of the two Transcripts."
RL Genomics 52:79-98(1998).
DR EMBL; Y14619; CAA74969.1; -.

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DR	EMBL; Y14620; CAA74969.1; JOINED.
DR	EMBL; Y14621; CAA74969.1; JOINED.
DR	EMBL; Y14622; CAA74969.1; JOINED.
DR	EMBL; Y14623; CAA74969.1; JOINED.
DR	EMBL; Y14624; CAA74969.1; JOINED.
DR	HSSP; P19438; INCF.
DR	InterPro: IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 4.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
DR	PROSITE; PS00652; TNFR_NGFR_2; 3.
KW	Receptor.
SQ	SEQUENCE 482 AA; 51106 MW; F6C15045B48FF83C CRC64;

Query Match		7.6%; Score 262.5; DB 11; Length 482;
Best Local Similarity		24.4%; Pred. No. 9.6e-13;
Matches	82; Conservative	33; Mismatches 128; Indels 93; Gaps 11;

Qy'	65	LTCDKCPAGYVVEHCTNT-----SLRVCSSCPVGTFTRHENGIEKCHDCSQPCWPMP	117
Dd	53	MCCAKPPGGYGVKHFCNKTSDTVCADSDTYACDEASMYTQVMNQFETCLSCSSCSSTDQ	112
Qy	118	IEXLPCAALTDRECTCPGPFGSNAT-----CAPHTVCPVGMGVKKGTETEDVRCKQ	170
Dd	113	VETRACKQNRCVACBAGRYCALKTHSGSCRCQLKPGCGFGVASSRAPNGNVLCKA	172
Qy	171	CARGTESDVPSSYMKKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSTSPSGTAIF	230
Dd	173	CAPGETSDDTSTSDVCRPHRIC---SILAIPGNASTDAVCA-----	210
Qy	231	PREHEMETHVPSSTYV----PKGMNSTESNASVRPKVLLSIQEGTVPDNTSSARGKE	286
Dd	211	--PESPFLSAIPTRLTYVSQPEPTRSRQDLDOEPGPSQTPIILTSI--GSTPIEQSTKG--	264
Qy	287	DVNKTLP-----NLQVVN-----HQQGH-----	305
Dd	265	--GISLPGLIVGVTSLGLMLGLNVCFILVQRKKPSCIQRDAKVHPHVDEKSQDQAVGL	322
Qy	306	-HRHILKLPSMEATGGEKSTPTI---KGPKRGRHP	337
Dd	323	EQQHLLTTAPSSSSSSLESSASAGDRRAPGGHPQ	358

RESULT 10
O72762 PRELIMINARY; PRT; 167 AA.
ID O72762 AC O72762; 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE K3R protein.
OS K3R.
GN Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RT smallpox, and vaccinia viruses.";
RL virology 243:432-460(1998)."
DR EMBL; Y15035; CAA73301.1; -.
DR HSSP; P19438; TEXT.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
SQ SEQUENCE 167 AA; 18526 MW; 384A0D5A67F73961 CRC64;

Db 179 DVEINLYPVNDTSCRTTTTGLSEISTSELTITMNHKDCDPVFRDGYFVSLMKVATSGF 238
QY 211 -----CGTLPSFSSTSPSPCTAIFPRPEHMETHEVPSSYVVK 249
Db 239 FTGENYQNLKSVCTLNFEIKCNKNDSSSKQLTKAKNDIMP---HSET-----VTLVGD 290
QY 250 GNMSTE-----SNSSASVRPKVLSSIQGTVPDNTSSARGKEDVNTLPNLQVYNH 300
Db 291 CLSSVDIYILYSNTQDYETDTSYHAGNVLDVDSHMPGSCDIHKLITNSQNP 346
CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_taxid=10243;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN-MUNICH Opv89/4(CAT);
RX MEDLINE=20579014; PubMed=11136755;
RA Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT detection and differentiation of old world orthopoxviruses;
RL restriction fragment length polymorphism of the crmb gene region.";
J. Clin. Microbiol. 39:94-100(2001).
DR EMBL; U90232; AAB94388.1; .
DR HSSP; O14763; 1DOG.
DR InterPro; IPR001388; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 38394 MW; 6D0E4040C0E9F78 CRC64;

RESULT 15

OS7121 PRELIMINARY; PRT; 351 AA.
AC 057121;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_taxid=10243;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN-MUNICH Opv89/4(CAT);
RX MEDLINE=20579014; PubMed=11136755;
RA Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT detection and differentiation of old world orthopoxviruses;
RL restriction fragment length polymorphism of the crmb gene region.";
J. Clin. Microbiol. 39:94-100(2001).
DR EMBL; U90232; AAB94388.1; .
DR HSSP; O14763; 1DOG.
DR InterPro; IPR001388; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 38394 MW; 6D0E4040C0E9F78 CRC64;
Query Match 6.7%; Score 233; DB 12; Length 351;
Best Local Similarity 24.9%; Pred. No. 1.5e-10;
Matches 82; Conservative 27; Mismatches 122; Indels 98; Gaps 11;
QY 54 YRHVDRATGQVLTCDKCPAGTYVSEHC---TNTSLRVSCSPVGTTRHENGIEKCHDCS 110
Db 37 YKH-----HHLCCSLCPPGTASRLCDSKTNTNQ-CTSCGSGTFTSRNNHLPACLSCN 89
QY 111 QPCPWPMEIKLPCAALTDRECTPPGMF-----QSNATCAPHTVCPVGWGVKKGTETE 164
Db 90 GRCDNQVETRSCNTHNRICECPGYCLLKSSGCKACVQTKCGMGYGV-SGHTSTG 148
QY 165 DVRCQCARGTFSVPSSVMKCKAY-----TDC-----LS 194
Db 149 DVICSPCGLGTYSHTVSSADKCEPVPNTFNIDVEINLYPVNDTSCRTTATGLSEIS 208
QY 195 QNLVVIKPGTKEIDNV-----CGTLPS 216
Db 209 TSELTITMNHKDCDPVFRDGYFVSLMKVATSGFTGENRYQNTSKVCTLNFEIKCNKDS 268
QY 217 FSSSTSPSPCTAIFPRPEHMETHEVPSSYVVKGMNSTE-----SNSSASVRPKVLSSIQ 271
Db 269 SSQQLTKNDTNP---HSET-----VTLVGDCLSSVDIYILYSNTQDYETDTSYH 320
QY 272 EGTVPDNTSSARGKEDVNTLPNLQVYNH 300
Db 321 AGNVLDVDSHMPGSCDIHKLITNSQNP 349

Search completed: July 11, 2003, 15:48:27
Job time : 41 secs

